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09/937779

TRANSMITTAL LETTER TO THE UNITED STATES

ATTORNEY'S DOCKET NUMBER 0093/000003

DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. 371

U.S. APPLICATION NO. (If known, see 37 CFR 1.5)

INTERNATIONAL APPLICATION NO.  
PCT/EP 00/02701

INTERNATIONAL FILING DATE  
12 OCT 2000

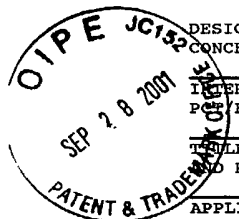
PRIORITY DATE CLAIMED  
March 28, 2000

TITLE OF INVENTION: A NEW CLASS OF ENZYMES IN THE BIOSYNTHETIC PATHWAY FOR THE PRODUCTION OF TRIACYLGLYCEROL AND RECOMBINANT DNA MOLECULES ENCODING THESE ENZYMES

APPLICANT(S) FOR DO/EO/US Anders DAHLQUIST; Ulf STAHL; Marit LENMAN; Antoni BANAS Hans RONNE; Sten STYMNE

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. /X/ This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.
  2. / / This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.
  3. /X/ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
  4. / / A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
  5. /X/ A copy of the International Application as filed (35 U.S.C. 371(c)(2)).
    - a. /X/ is transmitted herewith (required only if not transmitted by the International Bureau).
    - b. / / has been transmitted by the International Bureau.
    - c. / / is not required, as the application was filed in the United States Receiving Office (RO/USO).
  6. /X/ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
  7. / / Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)).
    - a. / / are transmitted herewith (required only if not transmitted by the International Bureau).
    - b. / / have been transmitted by the International Bureau.
    - c. / / have not been made; however, the time limit for making such amendments has NOT expired.
    - d. / / have not been made and will not be made.
  8. / / A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
  9. /X/ An oath or declaration of the inventor(s) (35 U.S.C. 171(c)(4)).
  10. / / A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).
- Items 11. to 16. below concern other document(s) or information included:
11. /X/ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
  12. / / An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
  13. /X/ A FIRST preliminary amendment.  
/ / A SECOND or SUBSEQUENT preliminary amendment.
  14. / / A substitute specification.
  15. / / A change of power of attorney and/or address letter.
  16. /X/ Other items or information.  
International Search Report  
International Preliminary Examination Report



JC05 Rec'd PCT/PTO 2 8 SEP 2001

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U.S. Appl. No. (If Known)	INTERNATIONAL APPLN. NO.	ATTORNEY'S DOCKET NO.
- - -	PCT/EP 00/02701	0093/000003

17. /X/ The following fees are submitted	<u>CALCULATIONS</u>	<u>PTO USE ONLY</u>
BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)):		
Search Report has been prepared by the		
EPO or JPO.....\$860.00	860.00	
International preliminary examination fee paid to USPTO		
(37 CFR 1.482).....\$690.00		
No international preliminary examination fee paid to		
USPTO (37 CFR 1.482) but international search fee paid		
to USPTO (37 CFR 1.445(a)(2)).....\$710.00		
Neither international preliminary examination fee		
(37 CFR 1.482) nor international search fee		
(37 CFR 1.445(a)(2)) paid to USPTO .....\$1000.00		
International preliminary examination fee paid to		
USPTO (37 CFR 1.482) and all claims satisfied pro		
-visions of PCT Article 33(2)-(4).....\$100.00		
ENTER APPROPRIATE BASIC FEE AMOUNT =	\$ 860.00	
Surcharge of \$130.00 for furnishing the oath or declaration		
later than / / 20 / / 30 months from the earliest		
claimed priority date (37 CFR 1.492(e)).		
<u>Claims</u>	<u>Number Filed</u>	<u>Number Extra</u>
Total Claims 22 -20	2	
Indep. Claims 4 -3	1	
Multiple dependent claim(s) (if applicable)		
	X\$18. 36.00	
	X\$80. 80.00	
	+270.	
TOTAL OF ABOVE CALCULATION	= 116.00	
Reduction of 1/4 for filing by small entity, if applicable.		
Verified Small Entity statement must also be filed		
(Note 37 CFR 1.9, 1.27, 1.28).		
SUBTOTAL	= 976.00	
Processing fee of \$130. for furnishing the English		
translation later than / / 20 / / 30 months from the		
earliest claimed priority date (37 CFR 1.492(f)). +		
TOTAL NATIONAL FEE	= 976.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)).		
The assignment must be accompanied by an appropriate cover		
sheet (37 CFR 3.28, 3.31) \$40.00 per property =		
TOTAL FEES ENCLOSED	= \$ 976.00	
Amount to be		
refunded:	\$	
Charged	\$	

- a./X/ A check in the amount of \$976.00 to cover the above fees is enclosed.
- b./ / Please charge my Deposit Account No. \_\_\_\_\_ in the amount of \$ \_\_\_\_\_ to cover the above fees. A duplicate copy of this sheet is enclosed.
- c./X/ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 11-0345. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:  
 KEIL & WEINKAUF  
 1101 Connecticut Ave., N.W.  
 Washington, D. C. 20036

*Herbert B. Keil*  
 \_\_\_\_\_  
 NAME  
 18,967  
 Registration No.

SIGNATURE

09/937779  
JC05 Rec'd PCT/PTO 2 8 SEP 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of )  
DAHLQUIST et al. )  
PCT/EP 00/02701 )  
Intl. Filing Date: March 28, 2000 )  
US Serial No.: TO BE ASSIGNED )

BOX PCT

For: A NEW CLASS OF ENZYMES IN THE BIOSYNTHETIC PATHWAY FOR THE  
PRODUCTION OF TRIACYLGLYCEROL AND RECOMBINANT DNA MOLECULES  
ENCODING THESE ENZYMES

Honorable Commissioner of  
Patents and Trademarks  
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Sir:

Prior to examination of the above-identified U.S. National  
Stage application, kindly amend the application as follows.

CLEAN VERSION OF ALL CLAIMS

Cancel claims 1-27, all the claims in this case, and substitute new claims 28-49 as follows:

28. An enzyme, designated as phospholipid:diacylglycerol acyltransferase (PDAT), catalyzing in an acyl-CoA-independent reaction the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol and comprising an amino acid sequence as set forth in SEQ ID NO:2 or a functional fragment, derivate, allele, homolog or isoenzyme thereof.

29. An enzyme according to claim 28, comprising an amino acid sequence encoded through a nucleotide sequence as set forth in SEQ ID NO:1 or a homologous nucleotide sequence which is at least about 40% identical to a nucleotide sequence of SEQ ID NO. 1.

30. An enzyme according to claim 28, comprising an amino acid sequence as set forth in SEQ ID NO. 16, 20 or 22, or a functional fragment, derivate, allele, homolog or isoenzyme thereof.

31. An enzyme according to claim 28, comprising an amino acid sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 6, 8, 13, 14, 15, 17, 18, 25 and 27, a functional fragment, derivate, allele, homolog or isoenzyme thereof.

32. An enzyme according to claim 28, comprising an amino acid sequence encoded through a nucleotide sequence, a portion, derivate, allele or homolog thereof selected from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31, or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence.

33. A nucleotide sequence according to claim 32, selected

from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 10, 11, 19, 21, 23, 24, 29 and 30, or a portion, derivate, allele or homolog thereof.

34. A partial nucleotide sequence corresponding to a full length nucleotide sequence according to claim 32, selected from the group consisting of sequences as set forth in SEQ ID NO. 5, 7, 9, 12, 25, 26, 28 and 31, or a portion, derivate, allele or homolog thereof.

35. A nucleotide sequence according to claim 32, comprising a nucleotide sequence which is at least 40% identical to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31.

36. A gene construct comprising a nucleotide sequence as set forth in SEQ ID No. 1, or a homologous nucleotide sequence which is at least about 40% identical to the nucleotide sequence of SEQ ID No. 1, which is operably linked to a heterologous nucleic.

37. A vector comprising a gene construct according to claim 36, or the nucleotide sequence as set forth in SEQ ID No. 1, or a homologous nucleotide sequence which is at least about 40% identical to the nucleotide sequence of SEQ ID No. 1.

38. A vector according to claim 37, which is an expression vector.

39. A vector according to claim 37, further comprising a selectable marker gene and/or nucleotide sequences for the replication in a host cell or the integration into the genome of the host cell.

40. A transgenic cell or organism comprising one or more of the following:

a) a nucleotide sequence  $a_1$  to  $a_4$ ),

b) a gene construct  $b_1$ ), and

c) a vector  $c_1$ ),

wherein

- $a_1$ ) is a nucleotide sequence as set forth in SEQ ID NO. 1 or a homologous nucleotide sequence which is at least about 40% identical to a nucleotide sequence of SEQ ID NO. 1,
- $a_2$ ) is a nucleotide sequence, a portion, derivate, allele or homolog thereof selected from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31, or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence,
- $a_3$ ) is a partial nucleotide sequence which corresponds to a full length nucleotide sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 5, 7, 9, 12, 25, 26, 28 or 31, or a portion, derivate, allele or homolog thereof;
- $a_4$ ) is a nucleotide sequence which is at least 40% identical to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31,
- $b_1$ ) is a gene construct comprising a nucleotide sequence  $a$ ), operably linked to a heterologous nucleic acid, and
- $c_1$ ) is a vector comprising a gene construct  $b_1$ ), or a nucleotide sequence  $a_1$ ).

41. A transgenic cell or organism according to claim 40, which is an eucaryotic cell or organism.

42. A transgenic cell or organism according to claim 40, which is a yeast cell or a plant cell or a plant.

43. A transgenic cell or organism according to claim 40 having an altered biosynthetic pathway for the production of

triacylglycerol, characterized by the prevention of accumulation of undesirable fatty acids, which are harmful if present in high amounts in membrane lipids.

44. A transgenic cell or organism according to claim 40 having an altered, increased oil content.

45. A transgenic cell or organism according to claim 40, wherein the activity of PDAT is altered, characterized by an alteration in gene expression, catalytic activity and/or regulation of activity of the enzyme.

46. A process for the production of triacylglycerol, comprising growing a transgenic cell or organism according to claim 40 under conditions whereby the said nucleotide sequence

- a<sub>1</sub>) is a nucleotide sequence as set forth in SEQ ID NO. 1 or a homologous nucleotide sequence which is at least about 40% identical to a nucleotide sequence of SEQ ID NO. 1,
  - a<sub>2</sub>) is a nucleotide sequence, a portion, derivate, allele or homolog thereof selected from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31, or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence,
  - a<sub>3</sub>) is a partial nucleotide sequence which corresponds to a full length nucleotide sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 5, 7, 9, 12, 25, 26, 28 or 31, or a portion, derivate, allele or homolog thereof;
  - a<sub>4</sub>) is a nucleotide sequence which is at least 40% identical to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31,
- is expressed.

47. Triacylglycerols produced by a process according to claim 46.

48. Use of a nucleotide sequence selected from the group of  
a<sub>1</sub>) is a nucleotide sequence as set forth in SEQ ID NO. 1 or a homologous nucleotide sequence which is at least about 40% identical to a nucleotide sequence of SEQ ID NO. 1,

a<sub>2</sub>) is a nucleotide sequence, a portion, derivate, allele or homolog thereof selected from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31, or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence,

a<sub>3</sub>) is a partial nucleotide sequence which corresponds to a full length nucleotide sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 5, 7, 9, 12, 25, 26, 28 or 31, or a portion, derivate, allele or homolog thereof;

a<sub>4</sub>) is a nucleotide sequence which is at least 40% identical to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31,

or an enzyme selected from the group of

d<sub>1</sub>) is an enzyme, designated as phospholipid:diacylglycerol acyltransferase (PDAT), catalyzing in an acyl-CoA-independent reaction the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol and comprising an amino acid sequence as set forth in SEQ ID NO. 2 or a functional fragment, derivate, allele, homolog or isoenzyme thereof,

d<sub>2</sub>) is an enzyme d), comprising an amino acid sequence as set forth in SEQ ID NO. 16, 20 or 22, or a functional fragment,



derivate, allele, homolog or isoenzyme thereof,  
d<sub>3</sub>) is an enzyme d<sub>1</sub>), comprising an amino acid sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 6, 8, 13, 14, 15, 17, 18, 25 and 27, or a functional fragment, derivate, allele, homolog or isoenzyme thereof, for the production of triacylglycerol and/or triacylglycerols with uncommon fatty acids, comprising medium chain fatty acids, hydroxylated fatty acids, epoxygenated fatty acids and acetylenic fatty acids.

49. Use of a nucleotide sequence selected from the group of
- a<sub>1</sub>) is a nucleotide sequence as set forth in SEQ ID NO. 1 or a homologous nucleotide sequence which is at least about 40% identical to a nucleotide sequence of SEQ ID NO. 1,
  - a<sub>2</sub>) is a nucleotide sequence, a portion, derivate, allele or homolog thereof selected from the group consisting of sequences as set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31, or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence,
  - a<sub>3</sub>) is a partial nucleotide sequence which corresponds to a full length nucleotide sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 5, 7, 9, 12, 25, 26, 28 or 31, or a portion, derivate, allele or homolog thereof;
  - a<sub>4</sub>) is a nucleotide sequence which is at least 40% identical to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 and 31,
- or an enzyme selected from the group of
- d<sub>1</sub>) is an enzyme, designated as phospholipid:diacylglycerol acyltransferase (PDAT), catalyzing in an acyl-CoA-independent

reaction the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol and comprising an amino acid sequence as set forth in SEQ ID NO. 2 or a functional fragment, derivate, allele, homolog or isoenzyme thereof,

d<sub>2</sub>) is an enzyme d<sub>1</sub>), comprising an amino acid sequence as set forth in SEQ ID NO. 16, 20 or 22, or a functional fragment, derivate, allele, homolog or isoenzyme thereof,

d<sub>3</sub>) is an enzyme d<sub>1</sub>), comprising an amino acid sequence selected from the group consisting of sequences as set forth in SEQ ID NO. 6, 8, 13, 14, 15, 17, 18, 25 and 27, or a functional fragment, derivate, allele, homolog or isoenzyme thereof,

for the transformation of any cell or organism in order to be expressed in this cell or organism and result in an altered, preferably increased oil content of this cell or organism.

REMARKS

The claims have been amended to eliminate multiple dependency and to place them in better form for U.S. practice. Further, amendments made in the international stage, albeit not under Article 19, are also incorporated. The changes made in the claims were as follows:

- i. the subject-matter of claim 2 and 3 was included in claim 1 (now claim 28);
- ii. claim 29 was introduced according to the disclosed homologous nucleotide sequence on page 6 of the specification;
- iii. claims 7, 8 and 25 were deleted;
- iv. claims 30-42 essentially correspond to claims 4-6 and 9-18 of the international application;
- v. claim 23 was incorporated into claim 19, which is now claim 43;
- vi. claim 20, now 44, was amended by defining the altered oil content according to page 9, line 9;
- vii. claim 22 was incorporated into claim 21, which is now claim 45;
- viii. claim 46 essentially corresponds to claim 24 of the international application.
- ix. in claim 26, now 47, triacylglycerols with uncommon fatty acids were defined according to page 10, line 29;

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x. claim 48 essentially corresponds to claim 27 of the international application;

xi. in the other claims, editorial amendments were made.

Favorable action on the application is solicited.

Respectfully submitted,

KEIL & WEINKAUF



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HBK/kas

JC09 Rec'd PCT/PTO 07 JUN 2002



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Re Application of )

DAHLQUIST et al. )

BOX PCT

Serial No. 09/937,779 )

Filed: September 28, 2001 )

For: NEW CLASS OF ENZYMES IN THE BIOSYNTHETIC PATHWAY FOR THE  
PRODUCTION OF TRIACYCLOGLYCEROL AND RECOMBINANT DNA  
MOLECULES ENCODING THESE ENZYMES

I hereby certify that this correspondence is being deposited with the  
United States Postal Service as first class mail in an envelope  
addressed to Commissioner of Patents and Trademarks,  
Washington, D.C. 20231, on:

June 5, 2002

Date of Deposit Karen Stamper

Person Making Deposit

Signature

June 5, 2002

Date of Signature

Honorable Commissioner of  
Patents and Trademarks  
Washington, D.C. 20231

PRELIMINARY AMENDMENT  
AND  
RESPONSE TO NOTIFICATION OF MISSING REQUIREMENTS UNDER 35 USC 371

Sir:

In response to the Notification of Missing Requirements under 35 USC 371, a  
copy of the Sequence Listing in computer readable form is attached hereto. The  
content of the paper copy of the Sequence Listing and the copy of the Sequence Listing  
in computer readable form is the same, and includes no new matter.

IN THE SPECIFICATION

Delete the sequence listing in the specification on pages 1/58 to 58/58 and  
substitute with the attached replacement sequence listing on separate pages 1-52.

**REMARKS**

It is believed that by submitting the present amendment and sequence listing diskette, the application now fully complies with the requirements of 37 CFR 1.821-1.825. Favorable action by the examiner is solicited.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such account.

Respectfully submitted,

KEIL & WEINKAUF

06/13/2002 HKAYPAGH 00000090 110345 09937779  
01 FC:154 130.00 CH



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06/13/2002 HKAYPAGH 00000090 110345 09937779  
02 FC:965 84.00 CH

A NEW CLASS OF ENZYMES IN THE BIOSYNTHETIC PATHWAY FOR THE  
PRODUCTION OF TRIACYLGLYCEROL AND RECOMBINANT DNA  
MOLECULES ENCODING THESE ENZYMES

- 5 The present invention relates to the isolation, identification and characterization of recombinant DNA molecules encoding enzymes catalysing the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol.
- 10 Triacylglycerol (TAG) is the most common lipid-based energy reserve in nature. The main pathway for synthesis of TAG is believed to involve three sequential acyl-transfers from acyl-CoA to a glycerol backbone (1, 2). For many years, acyl-CoA : diacylglycerol acyltransferase (DAGAT), which catalyzes the third acyl transfer reaction, was thought to be the only unique enzyme involved in
- 15 TAG synthesis. It acts by diverting diacylglycerol (DAG) from membrane lipid synthesis into TAG (2). Genes encoding this enzyme were recently identified both in the mouse (3) and in plants (4, 5), and the encoded proteins were shown to be homologous to acyl-CoA : cholesterol acyltransferase (ACAT). It was also recently reported that another DAGAT exists in the oleaginous fungus
- 20 *Mortierella ramanniana*, which is unrelated to the mouse DAGAT, the ACAT gene family or to any other known gene (6).

The instant invention relates to novel type of enzymes and their encoding genes for transformation. More specifically, the invention relates to use of a

25 type of genes encoding a not previously described type of enzymes hereinafter designated phospholipid:diacylglycerol acyltransferases (PDAT), whereby this enzyme catalyses an acyl-CoA-independent reaction. The said type of genes expressed alone in transgenic organisms will enhance the total amount of oil (triacylglycerols) produced in the cells. The PDAT genes, in combination with a

30 gene for the synthesis of an uncommon fatty acid will, when expressed in transgenic organisms, enhance the levels of the uncommon fatty acids in the triacylglycerols.

There is considerable interest world-wide in producing chemical feedstock, such as fatty acids, for industrial use from renewable plant resources rather than non-renewable petrochemicals. This concept has broad appeal to manufacturers and consumers on the basis of resource conservation and provides significant opportunity to develop new industrial crops for agriculture.


There is a diverse array of unusual fatty acids in oils from wild plant species and these have been well characterised. Many of these acids have industrial potential and this has led to interest in domesticating relevant plant species to enable agricultural production of particular fatty acids.

Development in genetic engineering technologies combined with greater understanding of the biosynthesis of unusual fatty acids now makes it possible to transfer genes coding for key enzymes involved in the synthesis of a particular fatty acid from a wild species into domesticated oilseed crops. In this way individual fatty acids can be produced in high purity and quantities at moderate costs.

In all crops like rape, sunflower, oilpalm etc., the oil (i.e. triacylglycerols) is the most valuable product of the seeds or fruits and other compounds like starch, protein, and fibre is regarded as by-products with less value. Enhancing the quantity of oil per weight basis at the expense of other compounds in oil crops would therefore increase the value of crop. If genes, regulating the allocation of reduced carbon into the production of oil can be up-regulated, the cells will accumulate more oil on the expense of other products. Such genes might not only be used in already high oil producing cells, such as oil crops, but could also induce significant oil production in moderate or low oil containing crops such as e.g. soy, oat, maize, potato, sugarbeets, and turnips as well as in micro-organisms.

30

Summary of the invention





Many of the unusual fatty acids of interest, e.g. medium chain fatty acids, hydroxy fatty acids, epoxy fatty acids and acetylenic fatty acids, have physical properties that are distinctly different from the common plant fatty acids. The present inventors have found that, in plant species naturally accumulating these uncommon fatty acids in their seed oil (i.e. triacylglycerol), these acids are absent, or present in very low amounts in the membrane (phospho)lipids of the seed. The low concentration of these acids in the membrane lipids is most likely a prerequisite for proper membrane function and thereby for proper cell functions. One aspect of the invention is that seeds of transgenic crops can be made to accumulate high amounts of uncommon fatty acids if these fatty acids are efficiently removed from the membrane lipids and channelled into seed triacylglycerols.

The inventors have identified a novel class of enzymes in plants catalysing the transfer of fatty acids from phospholipids to diacylglycerol in the production of triacylglycerol through an acyl-CoA-independent reaction and that these enzymes (phospholipid:diacylglycerol acyltransferases, abbreviated as PDAT) are involved in the removal of hydroxylated, epoxygenated fatty acids, and probably also other uncommon fatty acids such as medium chain fatty acids, from phospholipids in plants.

This enzyme reaction was shown to be present in microsomal preparations from baker's yeast (*Saccharomyces cerevisiae*). The instant invention further pertains to an enzyme comprising an amino acid sequence as set forth in SEQ ID No. 2 or a functional fragment, derivate, allele, homolog or isoenzyme thereof. A so called 'knock out' yeast mutant, disrupted in the respective gene was obtained and microsomal membranes from the mutant was shown to totally lack PDAT activity. Thus, it was proved that the disrupted gene encodes a PDAT enzyme (SEQ ID NO. 1 and 2). Furtherm, this PDAT enzyme is characterized through the amino acid sequence as set forth in SEQ ID NO 2 containing a lipase motif of the conserved sequence string FXKWVEA.

The instant invention pertains further to an enzyme comprising an amino acid sequence as set forth in SEQ ID NO. 16, 20 or 22 or a functional fragment, derivate, allele, homolog or isoenzyme thereof.

Further genes and/or proteins of so far unknown function were identified and are contemplated within the scope of the instant invention. A gene from *Schizosaccharomyces pombe*, SPBC776.14 (SEQ ID NO. 3), a putative open reading frame CAA22887 of the SPBC776.14 (SEQ ID NO. 13) were identified. Further *Arabidopsis thaliana* genomic sequences (SEQ ID NO. 4, 10 and 11) coding for putative proteins were identified, as well as a putative open reading frame AAC80628 from the *A. thaliana* locus AC 004557 (SEQ ID NO. 14) and a putative open reading frame AAD10668 from the *A. thaliana* locus AC 003027 (SEQ ID NO. 15) were identified.

Also, a partially sequenced cDNA clone from *Neurospora crassa* (SEQ ID NO. 9) and a *Zea mays* EST (Extended Sequence Tac) clone (SEQ ID NO. 7) and corresponding putative amino acid sequence (SEQ ID NO. 8) were identified. Finally, two cDNA clones were identified, one *Arabidopsis thaliana* EST (SEQ ID NO. 5 and corresponding predicted amino acid sequence SEQ ID NO. 6) and a *Lycopersicon esculentum* EST clone (SEQ ID NO. 12) were identified. Further, enzymes designated as PDAT comprising an amino acid sequence selected from the group consisting of sequences as set forth in SEQ ID NO 6, 17, 18, 25 or 27 containing a lipase motif FXKWVEA are contemplated within the scope of the invention. Moreover, an enzyme comprising an amino acid sequence encoded through a nucleotide sequence, a portion, derivate, allele or homolog thereof selected from the group consisting of sequences as set forth in SEQ ID No. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 or 31 or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence are included within the scope of the invention.

A functional fragment of the instant enzyme is understood to be any polypeptide sequence which shows specific enzyme activity of a phospholipid:diacylglycerol acyltransferase (PDAT). The length of the functional fragment can for example vary in a range from about  $660 \pm 10$  amino acids to

660  $\pm$  250 amino acids, preferably from about 660  $\pm$  50 to 660  $\pm$ 100 amino acids, whereby the „basic number“ of 660 amino acids corresponds in this case to the polypeptide chain of the PDAT enzyme of SEQ ID NO. 2 encoded by a nucleotide sequence according to SEQ ID NO. 1. Consequently, the „basic number“ of functional fulllength enzyme can vary in correspondance to the encoding nucleotide sequence.

A portion of the instant nucleotide sequence is meant to be any nucleotide sequence encoding a polypeptid which shows specific activity of a phospholipid:diacylglycerol acyltransferase (PDAT). The length of the nucleotide portion can vary in a wide range of about several hundreds of nucleotides based upon the coding region of the gene or a highly conserved sequence. For example the length varies in a range from about 1900  $\pm$  10 to 1900  $\pm$  1000 nucleotides, preferably from about 1900  $\pm$  50 to 1900  $\pm$ 700 and more preferably from about 1900  $\pm$  100 to 1900  $\pm$  500 nucleotides. whereby the „basic number“ of 1900 nucleotides corresponds in this case to the encoding nucleotide sequence of the PDAT enzyme of SEQ ID NO. 1. Consequently, the „basic number“ of functional fulllength gene can vary.

An allelic variant of the instant nucleotide sequence is understood to be any different nucleotide sequence which encodes a polypeptide with a functionally equivalent function. The alleles pertain naturally occurring variants of the instant nucleotide sequences as well as synthetic nucleotide sequences produced by methods known in the art. Contemplated are even altered nucleotide sequences which result in an enzyme with altered activity and/or regulation or which is resistant against specific inhibitors. The instant invention further includes natural or synthetic mutations of the originally isolated nucleotide sequences. These mutations can be substitution, addition, deletion, inversion or insertion of one or more nucleotides.

A homologous nucleotide sequence is understood to be a complementary sequence and/or a sequence which specifically hybridizes with the instant nucleotide sequence. Hybridizing sequences include similar sequences selected from the group of DNA or RNA which specifically interact to the instant

nucleotide sequences under at least moderate stringency conditions which are known in the art. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-  
5 65°C. This further includes short nucleotide sequences of e.g. 10 to 30 nucleotides, preferably 12 to 15 nucleotides. Included are also primer or hybridization probes.

A homologous nucleotide sequence included within the scope of the instant  
10 invention is a sequence which is at least about 40%, preferably at least about 50 % or 60%, and more preferably at least about 70%, 80% or 90% and most preferably at least about 95%, 96%, 97%, 98% or 99% or more homologous to a nucleotide sequence of SEQ ID NO. 1.

All of the aforementioned definitions are true for amino acid sequences and  
15 functional enzymes and can easily transferred by a person skilled in the art.

Isoenzymes are understood to be enzymes which have the same or a similar substrate specificity and/or catalytic activity but a different primary structure.

20 In a first embodiment, this invention is directed to nucleic acid sequences that encode a PDAT. This includes sequences that encode biologically active PDATs as well as sequences that are to be used as probes, vectors for transformation or cloning intermediates. The PDAT encoding sequence may encode a complete or partial sequence depending upon the intended use. All or  
25 a portion of the genomic sequence, cDNA sequence, precursor PDAT or mature PDAT is intended.

Further included is a nucleotide sequence selected from the group consisting of sequences set forth in SEQ ID No. 1, 3, 4, 10, 11, 19, 21, 23, 24, 29 or 30 or a  
30 portion, derivate, allele or homolog thereof. The invention pertains a partial nucleotide sequence corresponding to a fulllength nucleotide sequence selected from the group consisting of sequences set forth in SEQ ID No. 5, 7, 9, 12, 25, 26, 28 or 31 or a portion, derivate, allele or homolog thereof. Moreover, a

nucleotide sequence comprising a nucleotide sequence which is at least 40% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID No. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 or 31 is contemplated within the scope of the invention.

5

The instant invention pertains to a gene construct comprising a said nucleotide sequences of the instant invention which is operably linked to a heterologous nucleic acid.

The term operably linked means a serial organisation e.g. of a promotor, coding  
10 sequence, terminator and/or further regulatory elements whereby each element can fulfill its original function during expression of the nucleotide sequence.

Further, a vector comprising of a said nucleotide sequence of the instant invention is contemplated in the instant invention. This includes also an  
15 expression vector as well as a vector further comprising a selectable marker gene and/or nucleotide sequences for the replication in a host cell and/or the integration into the genome of the host cell.

In a different aspect, this invention relates to a method for producing a PDAT in  
20 a host cell or progeny thereof, including genetically engineered oil seeds, yeast and moulds or any other oil accumulating organism, via the expression of a construct in the cell. Cells containing a PDAT as a result of the production of the PDAT encoding sequence are also contemplated within the scope of the invention.

25

Further, the invention pertains a transgenic cell or organism containing a said nucleotide sequence and/or a said gene construct and/or a said vector. The object of the instant invention is further a transgenic cell or organism which is an eucaryotic cell or organism. Preferably, the transgenic cell or organism is a  
30 yeast cell or a plant cell or a plant. The instant invention further pertains said transgenic cell or organism having an altered biosynthetic pathway for the production of triacylglycerol. A transgenic cell or organism having an altered oil content is also contemplated within the scope of this invention.

Further, the invention pertains a transgenic cell or organism wherein the activity of PDAT is altered in said cell or organism. This altered activity of PDAT is characterized by an alteration in gene expression, catalytic activity and/or regulation of activity of the enzyme. Moreover, a transgenic cell or organism is included in the instant invention, wherein the altered biosynthetic pathway for the production of triacylglycerol is characterized by the prevention of accumulation of undesirable fatty acids in the membrane lipids.

10 In a different embodiment, this invention also relates to methods of using a DNA sequence encoding a PDAT for increasing the oil-content within a cell.

Another aspect of the invention relates to the accommodation of high amounts of uncommon fatty acids in the triacylglycerol produced within a cell, by introducing a DNA sequence producing a PDAT that specifically removes these fatty acids from the membrane lipids of the cell and channel them into triacylglycerol. Plant cells having such a modification are also contemplated herein.

20 Further, the invention pertains a process for the production of triacylglycerol, comprising growing a said transgenic cell or organism under conditions whereby the said nucleotide sequence is expressed and whereby the said transgenic cells comprising a said enzyme catalysing the transfer of fatty acids from phospholipids to diacylglycerol forming triacylglycerol.

25 Moreover, triacylglycerols produced by the aforementioned process are included in scope of the instant invention.

Object of the instant invention is further the use of an instant nucleotide sequence and/or a said enzyme for the production of triacylglycerol and/or triacylglycerols with uncommon fatty acids. The use of a said instant nucleotide sequence and/or a said enzyme of the instant invention for the transformation of any cell or organism in order to be expressed in this cell or organism and

30

result in an altered, preferably increased oil content of this cell or organism is also contemplated within the scope of the instant invention.

A PDAT of this invention includes any sequence of amino acids, such as a  
5 protein, polypeptide or peptide fragment obtainable from a microorganism,  
animal or plant source that demonstrates the ability to catalyse the production  
of triacylglycerol from a phospholipid and diacylglycerol under enzyme reactive  
conditions. By „enzyme reactive conditions“ is meant that any necessary  
conditions are available in an environment (e.g., such factors as temperature,  
10 pH, lack of inhibiting substances) which will permit the enzyme to function.

Other PDATs are obtainable from the specific sequences provided herein.  
Furthermore, it will be apparent that one can obtain natural and synthetic  
PDATs, including modified amino acid sequences and starting materials for  
15 synthetic-protein modelling from the exemplified PDATs and from PDATs which  
are obtained through the use of such exemplified sequences. Modified amino  
acid sequences include sequences that have been mutated, truncated,  
increased and the like, whether such sequences were partially or wholly  
synthesised. Sequences that are actually purified from plant preparations or  
20 are identical or encode identical proteins thereto, regardless of the method  
used to obtain the protein or sequence, are equally considered naturally  
derived.

Further, the nucleic acid probes (DNA and RNA) of the present invention can  
25 be used to screen and recover „homologous“ or „related“ PDATs from a variety  
of plant and microbial sources.

Further, it is also apparent that a person skilled in the art can, with the  
information provided in this application, in any organism identify a PDAT  
30 activity, purify an enzyme with this activity and thereby identify a „non-  
homologous“ nucleic acid sequence encoding such an enzyme.

The present invention can be essentially characterized by the following aspects:

1. Use of a PDAT gene (genomic clone or cDNA) for transformation.
- 5 2. Use of a DNA molecule according to item 1 wherein said DNA is used for transformation of any organism in order to be expressed in this organism and result in an active recombinant PDAT enzyme in order to increase oil content of the organism.
3. Use of a DNA molecule of item 1 wherein said DNA is used for  
10 transformation of any organism in order to prevent the accumulation of undesirable fatty acids in the membrane lipids.
4. Use according to item 1, wherein said PDAT gene is used for transforming transgenic oil accumulating organisms engineered to produce any uncommon fatty acid which is harmful if present in high amounts in  
15 membrane lipids, such as medium chain fatty acids, hydroxylated fatty acids, epoxygenated fatty acids and acetylenic fatty acids.
5. Use according to item 1, wherein said PDAT gene is used for transforming organisms, and wherein said organisms are crossed with other oil accumulating organisms engineered to produce any uncommon fatty acid  
20 which is harmful if present in high amounts in membrane lipids, comprising medium chain fatty acids, hydroxylated fatty acids, epoxygenated fatty acids and acetylenic fatty acids.
6. Use according to item 1, wherein the enzyme encoded by said PDAT gene or cDNA is coding for a PDAT with distinct acyl specificity.
- 25 7. Use according to item 1 wherein said PDAT encoding gene or cDNA, is derived from *Saccharomyces cerevisiae*, or contain nucleotide sequences coding for an amino acid sequence 30% or more identical to the amino acid sequence of PDAT as presented in SEQ. ID. NO. 2.
8. Use according to item 1 wherein said PDAT encoding gene or cDNA is  
30 derived from *Saccharomyces cerevisiae*, or contain nucleotide sequences coding for an amino acid sequence 40% or more identical to the amino acid sequence of PDAT as presented in SEQ. ID. NO. 2.



9. Use according to item 1 wherein said PDAT encoding gene or cDNA is derived from *Saccharomyces cerevisiae*, or contain nucleotide sequences coding for an amino acid sequence 60% or more *identical* to the amino acid sequence of PDAT as presented in SEQ. ID. NO. 2.
- 5 10. Use according to item 1 wherein said PDAT encoding gene or cDNA is derived from *Saccharomyces cerevisiae*, or contain nucleotide sequences coding for an amino acid sequence 80% or more identical to the amino acid sequence of PDAT as presented in SEQ. ID. NO. 2.
- 10 11. Use according to item 1 wherein said PDAT encoding gene or cDNA is derived from plants or contain nucleotide sequences coding for an amino acid sequence 40% or more identical to the amino acid sequence of PDAT from *Arabidopsis thaliana* or to the protein encoded by the fulllength counterpart of the partial Zea mays, Lycopersicon esculentum, or Neurospora crassa cDNA clones.
- 15 12. Transgenic oil accumulating organisms comprising, in their genome, a PDAT gene transferred by recombinant DNA technology or somatic hybridization.
13. Transgenic oil accumulating organisms according to item 12 comprising, in their genome, a PDAT gene having specificity for substrates with a particular uncommon fatty acid and the gene for said uncommon fatty acid.
- 20 14. Transgenic organisms according to item 12 or 13 which are selected from the group consisting of fungi, plants and animals.
15. Transgenic organisms according to item 12 or 13 which are selected from the group of agricultural plants.
- 25 16. Transgenic organisms according to item 12 or 13 which are selected from the group of agricultural plants and where said PDAT gene is expressed under the control of a storage organ specific promotor.
17. Transgenic organisms according to item 12 or 13 which are selected from the group of agricultural plants and where said PDAT gene is expressed under the control of a seed promotor.
- 30 18. Oils from organisms according to item 12 – 17.
19. A method for altering acyl specificity of a PDAT by alteration of the nucleotide sequence of a naturally occurring encoding gene and as a

consequence of this alternation creating a gene encoding for an enzyme with novel acyl specificity.

20. A protein encoded by a DNA molecule according to item 1 or a functional fragment thereof.
- 5 21. A protein of item 20 designated phospholipid:diacylglycerol acyltransferase.
22. A protein of item 21 which has a distinct acyl specificity.
23. A protein of item 13 having the amino acid sequence as set forth in SEQ, ID NO. 2, 13, 14 or 15 (and the proteins encoded by the fulllength or partial genes set forth in SEQ. ID. NO. 1, 3, 4, 5, 7, 9, 10, 11 or 12) or an amino
- 10 acid sequence with at least 30 % homology to said amino acid sequence.
24. A protein of item 23 isolated from *Saccharomyces cerevisiae*.

15

20 General methods:

Yeast strains and plasmids. The wild type yeast strains used were either FY1679 (*MAT $\alpha$  his3- $\Delta$ 200 leu2- $\Delta$ 1 trp1- $\Delta$ 6 ura3-52*) or W303-1A (*MAT $\alpha$  ADE2-1 can1-100 his3-11,15 leu2-3,112 trp1-1 ura3-1*) (7). The YNR008w::KanMX2 disruption strain FVKT004-04C(AL), which is congenic to FY1679, was

25 obtained from the Euroscarf collection (8). A 2751 bp fragment containing the YNR008w gene with 583 bp of 5' and 183 bp of 3' flanking DNA was amplified from W303-1A genomic DNA using *Taq* polymerase with 5'-TCTCCATCTTCTGCAAAACCT-3' and 5'-CCTGTCAAAAACCTTCTCCTC-3' as primers. The resulting PCR product was purified by agarose gel electrophoresis

30 and cloned into the *EcoRV* site of pBluescript (pbluescript-pdat). For complementation experiments, the cloned fragment was released from pBluescript by *HindIII*-*SacI* digestion and then cloned between the *HindIII* and *SacI* sites of pFL39 (9), thus generating pUS1. For overexpression of the PDAT

gene, a 2202 bp *EcoRI* fragment from the pBluscript plasmid which contains only 24 bp of 5' flanking DNA was cloned into the *BamHI* site of the *GAL1-TPK2* expression vector pJN92 (12), thus generating pUS4.

5        Microsomal preparations. Microsomes from developing seeds of sunflower (*Helianthus annuus*), *Ricinus communis* and *Crepis palaestina* were prepared using the procedure of Stobart and Stymne (11). To obtain yeast microsomes, 1g of yeast cells (fresh weight) was re-suspended in 8 ml of ice-cold buffer (20 mM Tris-Cl, pH 7.9, 10 mM MgCl<sub>2</sub>, 1 mM EDTA, 5 % (v/v) glycerol, 1 mM DTT,  
10 0.3 M ammonium sulfate) in a 12 ml glass tube. To this tube, 4 ml of glass beads (diameter 0.45-0.5 mm) were added, and the tube was then heavily shaken (3 x 60 s) in an MSK cell homogenizer (B. Braun Melsungen AG, Germany). The homogenized suspension was centrifuged at 20,000 x g for 15 min at 6°C and the resulting supernatant was again centrifuged at 100,000 x g  
15 for 2 h at 6°C. The 100,000 x g pellet was resuspended in 0.1 M potassium phosphate (pH 7.2), and stored at -80°C. It is subsequently referred to as the crude yeast microsomal fraction.

Lipid substrates. Radio-labeled ricinoleic (12-hydroxy-9-octadecenoic) and  
20 vernolic (12,13-epoxy-9-octadecenoic) acids were synthesized enzymatically from [1-<sup>14</sup>C]oleic acid and [1-<sup>14</sup>C]linoleic acid, respectively, by incubation with microsomal preparations from seeds of *Ricinus communis* and *Crepis palaestina*, respectively (12). The synthesis of phosphatidylcholines (PC) or phosphatidylethanolamines (PE) with <sup>14</sup>C-labeled acyl groups in the *sn*-2  
25 position was performed using either enzymatic (13), or synthetic (14) acylation of [<sup>14</sup>C]oleic, [<sup>14</sup>C]ricinoleic, or [<sup>14</sup>C]vernolic acid. Dioleoyl-PC that was labeled in the *sn*-1 position was synthesized from *sn*-1-[<sup>14</sup>C]oleoyl-lyso-PC and unlabeled oleic acid as described in (14). *Sn*-1-oleoyl-*sn*-2-[<sup>14</sup>C]ricinoleoyl-DAG was synthesized from PC by the action of phospholipase C type XI from *B.*  
30 *Cereus* (Sigma Chemical Co.) as described in (15). Monovernoloyl- and divernoloyl-DAG were synthesized from TAG extracted from seeds of *Euphorbia lagascae*, using the TAG-lipase (*Rizhopus arrizus*, Sigma Chemical

Co.) as previously described (16). Monoricinoleoyl-TAG was synthesized according to the same method using TAG extracted from Castor bean.

Lipid analysis. Total lipid composition of yeast were determined from cells  
5 harvested from a 40 ml liquid culture, broken in a glass-bead shaker and  
extracted into chloroform as described by Bligh and Dyer (17), and then  
separated by thin layer chromatography in hexane/diethylether/acetic acid  
(80:20:1) using pre-coated silica gel 60 plates (Merck). The lipid areas were  
located by brief exposure to  $I_2$  vapors and identified by means of appropriate  
10 standards. Polar lipids, sterol-esters and triacylglycerols, as well as the  
remaining minor lipid classes, referred to as other lipids, were excised from the  
plates. Fatty acid methylesters were prepared by heating the dry excised  
material at 85 °C for 60 min in 2% (v/v) sulfuric acid in dry methanol. The  
methyl esters were extracted with hexane and analyzed by GLC through a 50 m  
15 x 0.32 mm CP-Wax58-CB fused-silica column (Chrompack), with  
methylheptadecanoic acid as an internal standard. The fatty acid content of  
each fraction was quantified and used to calculate the relative amount of each  
lipid class. In order to determine the total lipid content, 3 ml aliquots from yeast  
cultures were harvested by centrifugation and the resulting pellets were washed  
20 with distilled water and lyophilized. The weight of the dried cells was  
determined and the fatty acid content was quantified by GLC-analyses after  
conversion to methylesters as described above. The lipid content was then  
calculated as nmol fatty acid (FA) per mg dry weight yeast.

25 Enzyme assays. Aliquots of crude microsomal fractions (corresponding to  
10 nmol of microsomal PC) from developing plant seeds or yeast cells were  
lyophilized over night.  $^{14}C$ -Labeled substrate lipids dissolved in benzene were  
then added to the dried microsomes. The benzene was evaporated under a  
stream of  $N_2$ , leaving the lipids in direct contact with the membranes, and 0.1  
30 ml of 50 mM potassium phosphate (pH 7.2) was added. The suspension was  
thoroughly mixed and incubated at 30°C for the time period indicated, up to 90  
min. Lipids were extracted from the reaction mixture using chloroform and  
separated by thin layer chromatography in hexane/diethylether/acetic acid

Acyl-CoA-independent synthesis of TAG by oil seed microsomes. A large number of unusual fatty acids can be found in oil seeds (20). Many of these fatty acids, such as ricinoleic (21) and vernolic acids (22), are synthesized using phosphatidylcholin (PC) with oleoyl or linoleoyl groups esterified to the *sn*-2 position, respectively, as the immediate precursor. However, even though PC can be a substrate for unusual fatty acid synthesis and is the major membrane lipids in seeds, unusual fatty acids are rarely found in the membranes. Instead, they are mainly incorporated into the TAG. A mechanism for efficient and selective transfer of these unusual acyl groups from PC into TAG must therefore exist in oil seeds that accumulate such unusual fatty acids. This transfer reaction was biochemically characterized in seeds from castor bean (*Ricinus communis*) and *Crepis palaestina*, plants which accumulate high levels of ricinoleic and vernolic acid, respectively, and sunflower (*Helianthus annuus*), a plant which has only common fatty acids in its seed oil. Crude microsomal fractions from developing seeds were incubated with PC having <sup>14</sup>C-labeled oleoyl, ricinoleoyl or vernoloyl groups at the *sn*-2 position. After the incubation, lipids were extracted and analyzed by thin layer chromatography. We found that the amount of radioactivity that was incorporated into the neutral lipid fraction increased linearly over a period of 4 hours (data not shown). The distribution of [<sup>14</sup>C]acyl groups within the neutral lipid fraction was analyzed after 80 min (Fig. 1). Interestingly the amount and distribution of radioactivity

between different neutral lipids were strongly dependent both on the plant species and on the type of [ $^{14}\text{C}$ ]acyl chain. Thus, sunflower microsomes incorporated most of the label into DAG, regardless of the type of [ $^{14}\text{C}$ ]acyl group. In contrast, *R. communis* microsomes preferentially incorporated

5 [ $^{14}\text{C}$ ]ricinoleoyl and [ $^{14}\text{C}$ ]vernoloyl groups into TAG, while [ $^{14}\text{C}$ ]oleyl groups mostly were found in DAG. *C. palaestina* microsomes, finally, incorporated only

10 [ $^{14}\text{C}$ ]vernoloyl groups into TAG, with [ $^{14}\text{C}$ ]ricinoleoyl groups being found mostly as free fatty acids, and [ $^{14}\text{C}$ ]oleyl groups in DAG. This shows that the high *in vivo* levels of ricinoleic acid and vernolic acid in the TAG pool of *R. communis* and *C. palaestina*, respectively, can be explained by an efficient and selective transfer of the corresponding acyl groups from PC to TAG in these organisms.

The in-vitro synthesis of triacylglycerols in microsomal preparations of developing castor bean is summarized in table 1.

15

PDAT: a novel enzyme that catalyzes acyl-CoA independent synthesis of TAG. It was investigated if DAG could serve both as an acyl donor as well as an acyl acceptor in the reactions catalyzed by the oil seed microsomes. Therefore, unlabeled divernoloyl-DAG was incubated with either *sn*-1-oleoyl-

20 *sn*-2-[ $^{14}\text{C}$ ]ricinoleoyl-DAG or *sn*-1-oleoyl-*sn*-2-[ $^{14}\text{C}$ ]ricinoleoyl-PC in the presence of *R. communis* microsomes. The synthesis of TAG molecules containing both [ $^{14}\text{C}$ ]ricinoleoyl and vernoloyl groups was 5 fold higher when [ $^{14}\text{C}$ ]ricinoleoyl-PC served as acyl donor as compared to [ $^{14}\text{C}$ ]ricinoleoyl-DAG (fig.1B). These data strongly suggests that PC is the immediate acyl donor and

25 DAG the acyl acceptor in the acyl-CoA-independent formation of TAG by oil seed microsomes. Therefore, this reaction is catalyzed by a new enzyme which we call phospholipid : diacylglycerol acyltransferase (PDAT).

PDAT activity in yeast microsomes. Wild type yeast cells were cultivated

30 under conditions where TAG synthesis is induced. Microsomal membranes were prepared from these cells and incubated with *sn*-2-[ $^{14}\text{C}$ ]ricinoleoyl-PC and DAG and the  $^{14}\text{C}$ -labeled products formed were analyzed. The PC-derived [ $^{14}\text{C}$ ]ricinoleoyl groups within the neutral lipid fraction mainly were found in free

fatty acids or TAG, and also that the amount of TAG synthesized was dependent on the amount of DAG that was added to the reaction (Fig.2). The *in vitro* synthesis of TAG containing both ricinoleoyl and vernoloyl groups, a TAG species not present *in vivo*, from exogenous added *sn*-2-[<sup>14</sup>C]ricinoleoyl-PC and unlabelled vernoloyl-DAG (Fig. 2, lane 3) clearly demonstrates the existence of an acyl-CoA-independent synthesis of TAG involving PC and DAG as substrates in yeast microsomal membranes. Consequently, TAG synthesis in yeast can be catalyzed by an enzyme similar to the PDAT found in plants.

10 *The PDAT encoding gene in yeast.*

A gene in the yeast genome (YNR008w) is known, but nothing is known about the function of YNR008w, except that the gene is not essential for growth under normal circumstances. Microsomal membranes were prepared from the yeast strain FVKT004-04C(AL) (8) in which this gene with unknown function had been disrupted. PDAT activity in the microsomes were assayed using PC with radiolabelled fatty acids at the *sn*-2 position. The activity was found to be completely absent in the disruption strain (Fig. 2 lane 4). Significantly, the activity could be partially restored by the presence of YNR008w on the single copy plasmid pUS1 (Fig. 2 lane 5). Moreover, acyl groups of phosphatidylethanolamine (PE) were efficiently incorporated into TAG by microsomes from the wild type strain whereas no incorporation occurred from this substrate in the mutant strain (data not shown). This shows that YNR008w encodes a yeast PDAT which catalyzes the transfer of an acyl group from the *sn*-2 position of phospholipids to DAG, thus forming TAG. It should be noted that no cholesterol esters were formed from radioactive PC even in incubations with added ergosterols, nor were the amount of radioactive free fatty acids formed from PC affected by disruption of the YNR008w gene (data not shown). This demonstrates that yeast PDAT do not have cholesterol ester synthesising or phospholipase activities.

30

*Increased TAG content in yeast cells that overexpress PDAT.* The effect of overexpressing the PDAT-encoding gene was studied by transforming a wild type yeast strain with the pUS4 plasmid in which the gene is expressed from

the galactose-induced *GAL1:TPK2* promoter. Cells containing the empty expression vector were used as a control. The cells were grown in synthetic glycerol-ethanol medium, and expression of the gene was induced after either 2 hours (early log phase) or 25 hours (stationary phase) by the addition of galactose. The cells were then incubated for another 21 hours, after which they were harvested and assays were performed. We found that overexpression of PDAT had no significant effect on the growth rate as determined by the optical density. However, the total lipid content, measured as  $\mu\text{mol}$  fatty acids per mg yeast dry weight, was 47% (log phase) or 29% (stationary phase) higher in the PDAT overexpressing strain than in the control. Furthermore, the polar lipid and sterolester content was unaffected by overexpression of PDAT. Instead, the elevated lipid content in these cells is entirely due to an increased TAG content (Fig. 3A,B). Thus, the amount of TAG was increased by 2-fold in PDAT overexpressing early log phase cells and by 40% in stationary phase cells. It is interesting to note that a significant increase in the TAG content was achieved by overexpressing PDAT even under conditions (*i.e.* in stationary phase) where DAGAT is induced and thus contributes significantly to TAG synthesis. *In vitro* PDAT activity assayed in microsomes from the PDAT overexpressing strain was 7-fold higher than in the control strain, a finding which is consistent with the increased levels of TAG that we observed *in vivo* (Fig. 3C). These results clearly demonstrate the potential use of the PDAT gene in increasing the oil content in transgenic organisms.

Substrate specificity of yeast PDAT. The substrate specificity of yeast PDAT was analyzed using microsomes prepared from the PDAT overexpressing strain (see Fig. 4). The rate of TAG synthesis, under conditions given in figure 4 with di-oleoyl-PC as the acyl-donor, was 0.15 nmol per min and mg protein. With both oleoyl groups of PC labeled it was possible, under the given assay conditions, to detect the transfer of 11 pmol/min of [ $^{14}\text{C}$ ]oleoyl chain into TAG and the formation of 15 pmol/min of lyso-PC. In microsomes from the PDAT-deficient strain, no TAG at all and only trace amounts of lyso-PC was detected, strongly suggesting that yeast PDAT catalyses the formation of equimolar amounts of TAG and lyso-PC when supplied with PC and DAG as



substrates. The fact that somewhat more lyso-PC than TAG is formed can be explained by the presence of a phospholipase in yeast microsomes, which produces lyso-PC and unesterified fatty acids from PC.

5        The specificity of yeast PDAT for different acyl group positions was investigated by incubating the microsomes with di-oleoyl-PC carrying a [ $^{14}\text{C}$ ]acyl group either at the *sn*-1 position (Fig. 4A bar 2) or the *sn*-2 position (Fig. 4A bar 3). We found that the major  $^{14}\text{C}$ -labeled product formed in the former case was lyso-PC, and in the latter case TAG. We conclude that yeast  
10       PDAT has a specificity for the transfer of acyl groups from the *sn*-2 position of the phospholipid to DAG, thus forming *sn*-1-lyso-PC and TAG. Under the given assay conditions, trace amounts of  $^{14}\text{C}$ -labelled DAG is formed from the *sn*-1 labeled PC by the reversible action of a CDP-choline : choline phosphotransferase. This labeled DAG can then be further converted into TAG  
15       by the PDAT activity. It is therefore not possible to distinguish whether the minor amounts of labeled TAG that is formed in the presence of di-oleoyl-PC carrying a [ $^{14}\text{C}$ ]acyl group in the *sn*-1 position, is synthesized directly from the *sn*-1-labeled PC by a PDAT that also can act on the *sn*-1 position, or if it is first converted to *sn*-1-labeled DAG and then acylated by a PDAT with strict  
20       selectivity for the transfer of acyl groups at the *sn*-2 position of PC. Taken together, this shows that the PDAT encoded by YNR008w catalyses an acyl transfer from the *sn*-2 position of PC to DAG, thus causing the formation of TAG and lyso-PC.

25       The substrate specificity of yeast PDAT was further analyzed with respect to the headgroup of the acyl donor, the acyl group transferred and the acyl chains of the acceptor DAG molecule. The two major membrane lipids of *S. cerevisiae* are PC and PE, and as shown in Fig. 4B (bars 1 and 2), dioleoyl-PE is nearly 4-fold more efficient than dioleoyl-PC as acyl donor in the PDAT-catalyzed reaction. Moreover, the rate of acyl transfer is strongly dependent on  
30       the type of acyl group that is transferred. Thus, a ricinoleoyl group at the *sn*-2 position of PC is 2.5 times more efficiently transferred into TAG than an oleoyl group in the same position (Fig. 4B bars 1 and 3). In contrast, yeast PDAT has

no preference for the transfer of vernoloyl groups over oleoyl groups (Fig. 4B bars 1 and 4). The acyl chain of the acceptor DAG molecule also affects the efficiency of the reaction. Thus, DAG with a ricinoleoyl or a vernoloyl group is a more efficient acyl acceptor than dioleoyl-DAG (Fig. 4B bars 1, 5 and 6). Taken  
5 together, these results clearly show that the efficiency of the PDAT-catalyzed acyl transfer is strongly dependent on the properties of the substrate lipids.

PDAT genes. Nucleotide and amino acid sequences of several PDAT genes are given as SEQ ID No. 1 through 15. Further provisional and/or partial  
10 sequences are given as SEQ ID NO 16 through 20 and 21 through 31, respectively. One of the Arabidopsis genomic sequences (SEQ ID NO. 4) identified an Arabidopsis EST cDNA clone; T04806. This cDNA clone was fully characterised and the nucleotide sequence is given as SEQ ID NO. 5. Based  
15 on the sequence homology of the T04806 cDNA and the *Arabidopsis thaliana* genomic DNA sequence (SEQ ID NO 4) it is apparent that an additional A is present at position 417 in the cDNA clone (data not shown). Excluding this nucleotide would give the amino acid sequence depicted in SEQ ID NO. 12.

Increased TAG content in seeds of Arabidopsis thaliana that express the  
20 yeast PDAT. For the expression of the yeast PDAT gene in *Arabidopsis thaliana* an EcoRI fragment from the pBluescript-PDAT was cloned together with napin promotor (25) into the vector pGPTV-KAN (26). A plasmid (pGNapPDAT) having the yeast PDAT gene in the correct orientation was identified and transformed into *Agrobacterium tumefaciens*. These bacteria  
25 were used to transform *Arabidopsis thaliana* columbia (C-24) plants using the root transformation method (27). Plants transformed with an empty vector were used as controls.

First generation seeds (T1) were harvested and germinated on kanamycin containing medium. Second generation seeds (T2) were pooled from individual  
30 plants and their fatty acid contents analysed by quantification of their methyl esters by gas liquid chromatography after methylation of the seeds with 2% sulphuric acid in methanol at 85 °C for 1,5 hours. Quantification was done with heptadecanoic acid methyl esters as internal standard.

From the transformation with pGNapPDAT one T1 plant (26-14) gave raise to seven T2 plants of which 3 plants yielded seeds with statistically (in a mean difference two-sided test) higher oil content than seeds from T2 plants generated from T1 plant 32-4 transformed with an empty vector (table 2).

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- 10

## Description of Figures

FIG. 1.

Metabolism of  $^{14}\text{C}$ -labeled PC into the neutral lipid fraction by plant  
5 microsomes. (A) Microsomes from developing seeds of sunflower, *R.*  
*communis* and *C. palaestina* were incubated for 80 min at 30°C with PC (8  
nmol) having oleic acid in its *sn*-1 position, and either  $^{14}\text{C}$ -labeled oleic,  
ricinoleic or vernolic acid in its *sn*-2 position. Radioactivity incorporated in TAG  
(open bars), DAG (solid bars), and unsterified fatty acids (hatched bars) was  
10 quantified using thin layer chromatography followed by electronic  
autoradiography, and is shown as percentage of added labeled substrate. (B)  
Synthesis *in vitro* of TAG carrying two vernoloyl and one [ $^{14}\text{C}$ ]ricinoleoyl group  
by microsomes from *R. communis*. The substrates added were unlabeled  
divernoloyl-DAG (5 nmol), together with either *sn*-1-oleoyl-*sn*-2-[ $^{14}\text{C}$ ]ricinoleoyl-  
15 DAG (0.4 nmol, 7700 dpm/nmol) or *sn*-1-oleoyl-*sn*-2-[ $^{14}\text{C}$ ]ricinoleoyl-PC (0.4  
nmol, 7700 dpm/nmol). The microsomes were incubated with the substrates for  
30 min at 30°C, after which samples were removed for lipid analysis as  
described in the section „general methods“. The data shown are the average of  
two experiments.

20

FIG. 2.

PDAT activity in yeast microsomes, as visualized by autoradiogram of neutral  
lipid products separated on TLC. Microsomal membranes (10 nmol of PC) from  
the wild type yeast strain FY1679 (lanes 1-3), a congenic yeast strain  
25 (FVKT004-04C(AL)) that is disrupted for YNR008w (lane 4) or the same  
disruption strain transformed with the plasmid pUS1, containing the YNR008w  
gene behind its native promotor (lane 5), were assayed for PDAT activity. As  
substrates, we used 2 nmol *sn*-1-oleoyl-*sn*-2-[ $^{14}\text{C}$ ]ricinoleoyl-PC together with  
either 5 nmol of dioleoyl-DAG (lanes 2, 4 and 5) or *rac*-oleoyl-vernoleoyl-DAG  
30 (lane 3). The enzymatic assay and lipid analysis was performed as described in  
Materials and Methods. The cells were precultured for 20 h in liquid YPD  
medium, harvested and re-suspended in an equal volume of minimal medium  
(19) containing 16 g/l glycerol. The cells were then grown for an additional 24 h

prior to being harvested. Selection for the plasmid was maintained by growing the transformed cells in synthetic medium lacking uracil (18). Abbreviations: 1-OH-TAG, monoricinoleoyl-TAG; 1-OH-1-ep-TAG, monoricinoleoyl-monovernoloyl-TAG; OH-FA, unesterified ricinoleic acid.

5

Fig. 3.

Lipid content (A,B) and PDAT activity (C) in PDAT overexpressing yeast cells.

The PDAT gene in the plasmid pUS4 was overexpressed from the galactose-induced *GAL1-TPK2* promotor in the wild type strain W303-1A (7). Its expression was induced after (A) 2 hours or (B) 25 hours of growth by the addition of 2% final concentration (w/v) of galactose. The cells were then incubated for another 22 hours before being harvested. The amount of lipids of the harvested cells was determined by GLC-analysis of its fatty acid contents and is presented as  $\mu\text{mol}$  fatty acids per mg dry weight in either TAG (open bar), polar lipids (hatched bar), sterol esters (solid bar) and other lipids (striped bar). The data shown are the mean values of results with three independent yeast cultures. (C) *In vitro* synthesis of TAG by microsomes prepared from yeast cells containing either the empty vector (vector) or the PDAT plasmid (+ PDAT). The cells were grown as in Fig. 3A. The substrate lipids dioleoyl-DAG (2.5 nmol) and *sn*-1-oleoyl-*sn*-2- $^{14}\text{C}$ -oleoyl-PC (2 nmol) were added to aliquots of microsomes (10 nmol PC), which were then incubated for 10 min at 28 °C. The amount of label incorporated into TAG was quantified by electronic autoradiography. The results shown are the mean values of two experiments.

25 FIG. 4.

Substrate specificity of yeast PDAT. The PDAT activity was assayed by incubating aliquots of lyophilized microsomes (10 nmol PC) with substrate lipids at 30°C for 10 min (panel A) or 90 min (panel B). Unlabeled DAG (2.5 nmol) was used as substrates together with different labeled phospholipids, as shown in the figure. (A) *Sn*-position specificity of yeast PDAT regarding the acyl donor substrate. Dioleoyl-DAG together with either *sn*-1- $^{14}\text{C}$ -oleoyl-*sn*-2- $^{14}\text{C}$ -oleoyl-PC (di- $^{14}\text{C}$ -PC), *sn*-1- $^{14}\text{C}$ -oleoyl-*sn*-2-oleoyl-PC (*sn*1- $^{14}\text{C}$ -PC) or *sn*-1-oleoyl-*sn*-2- $^{14}\text{C}$ -oleoyl-PC (*sn*2- $^{14}\text{C}$ -PC). (B) Specificity of yeast PDAT regarding

30

phospholipid headgroup and of the acyl composition of the phospholipid as well as of the diacylglycerol. Dioleoyl-DAG together with either *sn*-1-oleoyl-*sn*-2-[<sup>14</sup>C]oleoyl-PC (oleoyl-PC), *sn*-1-oleoyl-*sn*-2-[<sup>14</sup>C]oleoyl-PE (oleoyl-PE), *sn*-1-oleoyl-*sn*-2-[<sup>14</sup>C]ricinoleoyl-PC (ricinoleoyl-PC) or *sn*-1-oleoyl-*sn*-2-[<sup>14</sup>C]vernoloyl-PC (vernoloyl-PC). In the experiments presented in the 2 bars to the far right, monoricinoleoyl-DAG (ricinoleoyl-DAG or mono-vernoloyl-DAG (vernoloyl-DAG) were used together with *sn*-1-oleoyl-*sn*-2-[<sup>14</sup>C]-oleoyl-PC. The label that was incorporated into TAG (solid bars) and lyso-PC (LPC, open bars) was quantified by electronic autoradiography. The results shown are the mean values of two experiments. The microsomes used were from W303-1A cells overexpressing the PDAT gene from the *GAL1-TPK2* promotor, as described in Fig. 3. The expression was induced at early stationary phase and the cells were harvested after an additional 24 h.

15

## TAB.1:

In vitro synthesis of triacylglycerols in microsomal preparations of developing castor bean. Aliquots of microsomes (20 nmol PC) were lyophilised and substrate lipids were added in benzene solution: (A) 0.4 nmol [<sup>14</sup>C]-DAG (7760 dpm/nmol) and where indicated 1.6 nmol unlabelled DAG; (B) 0.4 nmol [<sup>14</sup>C]-DAG (7760 dpm/nmol) and 5 nmol unlabelled di-ricinoleoyl-PC and (C) 0.25 nmol [<sup>14</sup>C]-PC (4000 dpm/nmol) and 5 nmol unlabelled DAG. The benzene was evaporated by N<sub>2</sub> and 0.1 ml of 50 mM potassium phosphate was added, thoroughly mixed and incubated at 30 °C for (A) 20 min.; (B) and (C) 30 min.. Assays were terminated by extraction of the lipids in chloroform. The lipids were then separated by thin layer chromatography on silica gel 60 plates (Merck; Darmstadt, Germany) in hexan/diethylether/acetic 35:70:1.5. The radioactive lipids were visualised and the radioactivity quantified on the plate by electronic autoradiography (Instant Imager. Packard, US). Results are presented as mean values of two experiments.

30

Radioactivity in different triacylglycerols (TAG) species formed. Abbreviations used: 1-OH-, mono-ricinoleoyl-; 2-OH-, di-ricinoleoyl-; 3-OH-, triricinoleoyl; 1-



OH-1-ver-, mono-ricinoleoyl-monovernoleoyl-; 1-OH-2-ver-, mono-ricinoleoyl-divernoleoyl-. Radiolabelled DAG and PC were prepared enzymatically. The radiolabelled ricinoleoyl group is attached at the sn-2-position of the lipid and unlabelled oleoyl group at the sn-1-position. Unlabelled DAG with vernoleoyl- or  
5 ricinoleoyl chains were prepared by the action of TAG lipase (6) on oil of Euphorbia lagascae or Castor bean, respectively. Synthetic di-ricinoleoyl-PC was kindly provided from Metapontum Agribios (Italy).

10 TAB.2:

Total fatty acids per mg of T2 seeds pooled from individual *Arabidopsis thaliana* plants transformed with yeast PDAT gene under the control of napin promotor (26-14) or transformed with empty vector (32-4).

15 \* = statistical difference between control plants and PDAT transformed plants in a mean difference two-sided test at  $\alpha = 5$ .

Description of the SEQ ID:

5     *SEQ ID NO. 1:* Genomic DNA sequence and suggested amino acid sequence of the *Saccharomyces cerevisiae* PDAT gene, YNR008w, with GenBank accession number Z71623 and Y13139, and with nucleotide ID number 1302481.

*SEQ ID NO. 2:* The amino acid sequence of the suggested open reading frame YNR008w from *Saccharomyces cerevisiae*.

10    *SEQ ID NO. 3:* Genomic DNA sequence of the *Schizosaccharomyces pombe* gene SPBC776.14.

*SEQ ID NO. 4:* Genomic DNA sequence of part of the *Arabidopsis thaliana* locus with GenBank accession number AB006704.

15

*SEQ ID NO. 5:* Nucleotide sequence of the *Arabidopsis thaliana* cDNA clone with GenBank accession number T04806, and nucleotide ID number 315966.

20    *SEQ ID NO. 6:* Predicted amino acid sequence of the *Arabidopsis thaliana* cDNA clone with GenBank accession number T04806.

*SEQ ID NO. 7:* Nucleotide and amino acid sequence of the *Zea mays* EST clone with GenBank accession number AI491339, and nucleotide ID number 4388167.

25    *SEQ ID NO. 8:* Predicted amino acid sequence of the *Zea mays* EST clone with GenBank accession number AI491339, and nucleotide ID number 4388167.

30    *SEQ ID NO. 9:* DNA sequence of part of the *Neurospora crassa* EST clone W07G1, with GenBank accession number AI398644, and nucleotide ID number 4241729.

*SEQ ID NO. 10:* Genomic DNA sequence of part of the *Arabidopsis thaliana* locus

with GenBank accession number AC004557.

*SEQ ID NO. 11:* Genomic DNA sequence of part of the *Arabidopsis thaliana* locus with GenBank accession number AC003027.

5

*SEQ ID NO. 12:* DNA sequence of part of the *Lycopersicon esculentum* cDNA clone with GenBank accession number AI486635.

*SEQ ID NO. 13:* Amino acid sequence of the *Schizosaccharomyces pombe* putative open reading frame CAA22887 of the *Schizosaccharomyces pombe* gene SPBC776.14.

10

*SEQ ID NO. 14:* Amino acid sequence of the *Arabidopsis thaliana* putative open reading frame AAC80628 derived from the *Arabidopsis thaliana* locus with GenBank accession number AC004557.

15

*SEQ ID NO 15:* Amino acid sequence of the *Arabidopsis thaliana* putative open reading frame AAD10668 derived from the *Arabidopsis thaliana* locus with GenBank accession number AC003027.

20

Further provisional and/or partial sequences are defined through the following SEQ IDs:

*SEQ ID NO. 16:* The amino acid sequence of the yeast ORF YNR008w from *Saccharomyces cerevisiae*.

25

*SEQ ID NO. 17:* Amino acid sequence of the region of the *Arabidopsis thaliana* genomic sequence (AC004557).

*SEQ ID NO. 18:* Amino acid sequence of the region of the *Arabidopsis thaliana* genomic sequence (AB006704).

30

SEQ ID NO. 19: The corresponding genomic DNA sequence and amino acid sequence of the yeast ORF YNROO8w from *Saccharomyces cerevisiae*.

5 SEQ ID NO. 20: The amino acid sequence of the yeast ORF YNROO8w from *Saccharomyces cerevisiae* derived from the corresponding genomic DNA sequence.

10 SEQ ID NO. 21: Genomic DNA sequence of the *Saccharomyces cerevisiae* PDAT gene, YNR008w, genebank nucleotide ID number 1302481, and the suggested YNR008w amino acid sequence.

15 SEQ ID NO. 22: The suggested amino acid sequence of the yeast gene YNR008w from *Saccharomyces cerevisiae*.

SEQ ID NO. 23: Genomic DNA sequence of the *Schizosaccharomyces pombe* gene SPBC776.14.

20 SEQ ID NO. 24: Genomic DNA sequence of part of the *Arabidopsis thaliana* locus with genebank accession number AB006704.

25 SEQ ID NO. 25: Nucleotide sequence and the corresponding amino acid sequence of the *Arabidopsis thaliana* EST-clone with genebank accession number T04806, and ID number 315966.

SEQ ID NO. 26: Nucleotide and amino acid sequence of the *Zea mays* cDNA clone with genebank ID number 4388167.

30 SEQ ID NO. 27: Amino acid sequence of the *Zea mays* cDNA clone with genebank ID number 4388167.

SEQ ID NO. 28: DNA sequence of part of the *Neurospora crassa* cDNA clone WO7G1, ID number 4241729.

*SEQ ID NO. 29:* Genomic DNA sequence of part of the *Arabidopsis thaliana* locus with genebank accession number AC004557.

- 5 *SEQ ID NO. 30:* Genomic DNA sequence of part of the *Arabidopsis thaliana* locus with genebank accession number AC003027.

*SEQ ID NO. 31:* DNA sequence of part of the *Lycopersicon esculentum* cDNA clone with genebank accession number AI486635.

**Claims**

1. An enzyme catalysing in an acyl-CoA-independent reaction the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway  
5 for the production of triacylglycerol.
2. An enzyme according to claim 1, comprising an amino acid sequence as set forth in SEQ ID No. 2 or a functional fragment, derivate, allele, homolog or isoenzyme thereof.  
10
3. An enzyme according to claims 1 or 2 designated as phospholipid:diacylglycerol acyltransferase (PDAT).
4. An enzyme according to claims 1 to 3, comprising an amino acid sequence  
15 as set forth in SEQ ID No. 16, 20 or 22 or a functional fragment, derivate, allele, homolog or isoenzyme thereof.
5. An enzyme according to claims 1 to 4, comprising an amino acid sequence selected from the group consisting of sequences as set forth in SEQ ID No.  
20 6, 8, 13, 14, 15, 17, 18, 25 or 27 or a functional fragment, derivate, allele, homolog or isoenzyme thereof.
6. An enzyme according to claims 1 to 5, comprising an amino acid sequence encoded through a nucleotide sequence, a portion, derivate, allele or  
25 homolog thereof selected from the group consisting of sequences as set forth in SEQ ID No. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 or 31 or a functional fragment, derivate, allele, homolog or isoenzyme of the enzyme encoding amino acid sequence.
- 30 7. A nucleotide sequence encoding an enzyme catalysing in an acyl-CoA-independent reaction the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol.

8. A nucleotide sequence according to claim 7 encoding an enzyme designated as phospholipid:diacylglycerol acyltransferase (PDAT).
- 5 9. A nucleotide sequence according to claims 7 or 8, selected from the group consisting of sequences as set forth in SEQ ID No. 1, 3, 4, 10, 11, 19, 21, 23, 24, 29 or 30 or a portion, derivate, allele or homolog thereof.
- 10 10. A partial nucleotide sequence corresponding to a fulllength nucleotide sequence according to claims 7 to 9, selected from the group consisting of sequences as set forth in SEQ ID No. 5, 7, 9, 12, 25, 26, 28 or 31 or a portion, derivate, allele or homolog thereof.
- 15 11. A nucleotide sequence according to claims 7 to 10, comprising a nucleotide sequence which is at least 40% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID No. 1, 3, 4, 5, 7, 9, 10, 11, 12, 19, 21, 23, 24, 25, 26, 28, 29, 30 or 31.
- 20 12. A gene construct comprising a nucleotide sequence according to claims 7 to 11 operably linked to a heterologous nucleic acid.
13. A vector comprising a nucleotide sequence according to claims 7 to 11 or a gene construct according to claim 12.
- 25 14. A vector according to claim 13, which is an expression vector.
15. A vector according to claims 13 or 14, further comprising a selectable marker gene and/or nucleotide sequences for the replication in a host cell or the integration into the genome of the host cell.
- 30 16. A transgenic cell or organism containing a nucleotide sequence according to claims 7 to 11 and/or a gene construct according to claim 12 and/or a vector according to claims 13 to 15.

17. A transgenic cell or organism according to claim 16 which is an eucaryotic cell or organism.
- 5 18. A transgenic cell or organism according to claims 16 or 17 which is a yeast cell or a plant cell or a plant.
19. A transgenic cell or organism according to claims 16 to 18 having an altered biosynthetic pathway for the production of triacylglycerol.
- 10 20. A transgenic cell or organism according to claims 16 to 19 having an altered oil content.
21. A transgenic cell or organism according to claims 16 to 20 wherein the  
15 activity of PDAT is altered.
22. A transgenic cell or organism according to claims 16 to 21 wherein the altered activity of PDAT is characterized by an alteration in gene expression, catalytic activity and/or regulation of activity of the enzyme.
- 20 23. A transgenic cell or organism according to claims 16 to 22 wherein the altered biosynthetic pathway for the production of triacylglycerol is characterized by the prevention of accumulation of undesirable fatty acids in the membrane lipids.
- 25 24. A process for the production of triacylglycerol, comprising growing a transgenic cell or organism according to claims 16 to 23 under conditions whereby the said nucleotide sequence according to claims 7 to 11 is expressed.
- 30 25. Triacylglycerols produced by a process according to claim 24.



26. Use of a nucleotide sequence according to claims 7 to 11 and/or an enzyme according to claims 1 to 6 for the production of triacylglycerol and/or triacylglycerols with uncommon fatty acids.
- 5 27. Use of a nucleotide sequence according to claims 7 to 11 and/or an enzyme according to claims 1 to 6 for the transformation of any cell or organism in order to be expressed in this cell or organism and result in an altered, preferably increased oil content of this cell or organism.

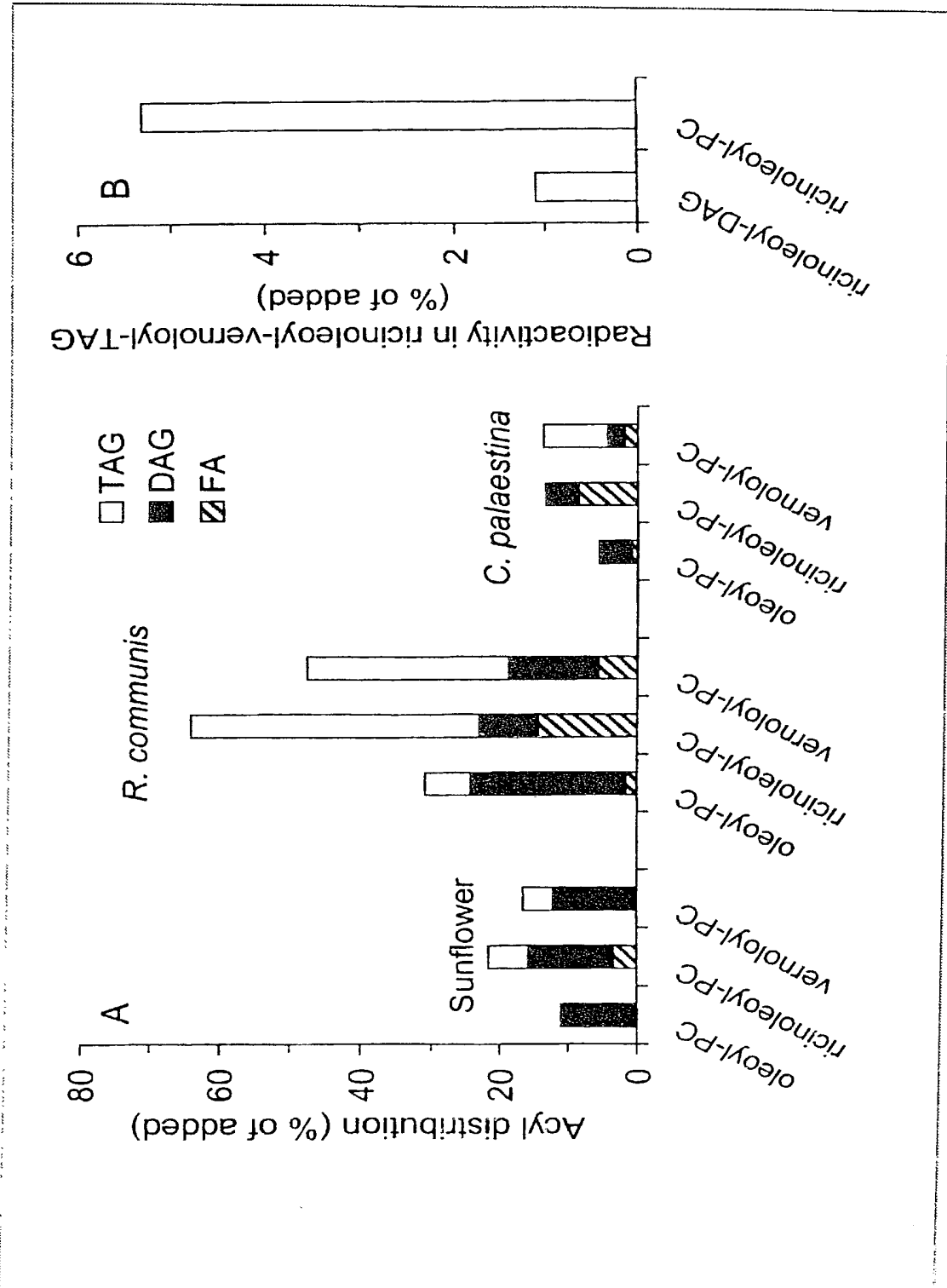
Abstract of the Disclosure

The present invention relates to the isolation, identification and characterization  
5 of nucleotide sequences encoding an enzyme catalysing the transfer of fatty  
acids from phospholipids to diacylglycerol in the biosynthetic pathway for the  
production of triacylglycerol, to the said enzymes and a process for the  
production of triacylglycerols.

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## Figures

Fig. 1:



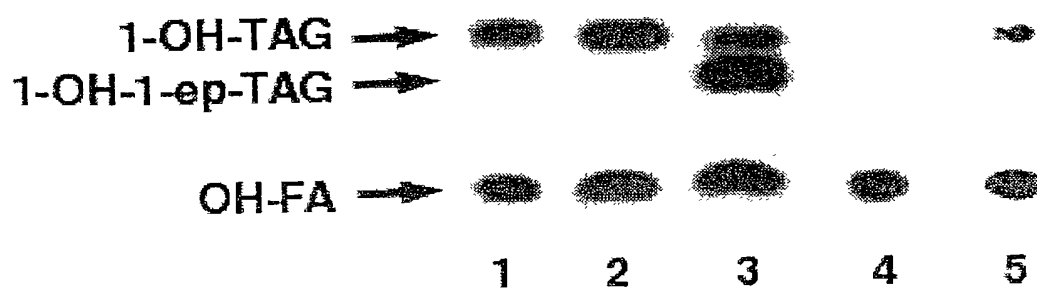
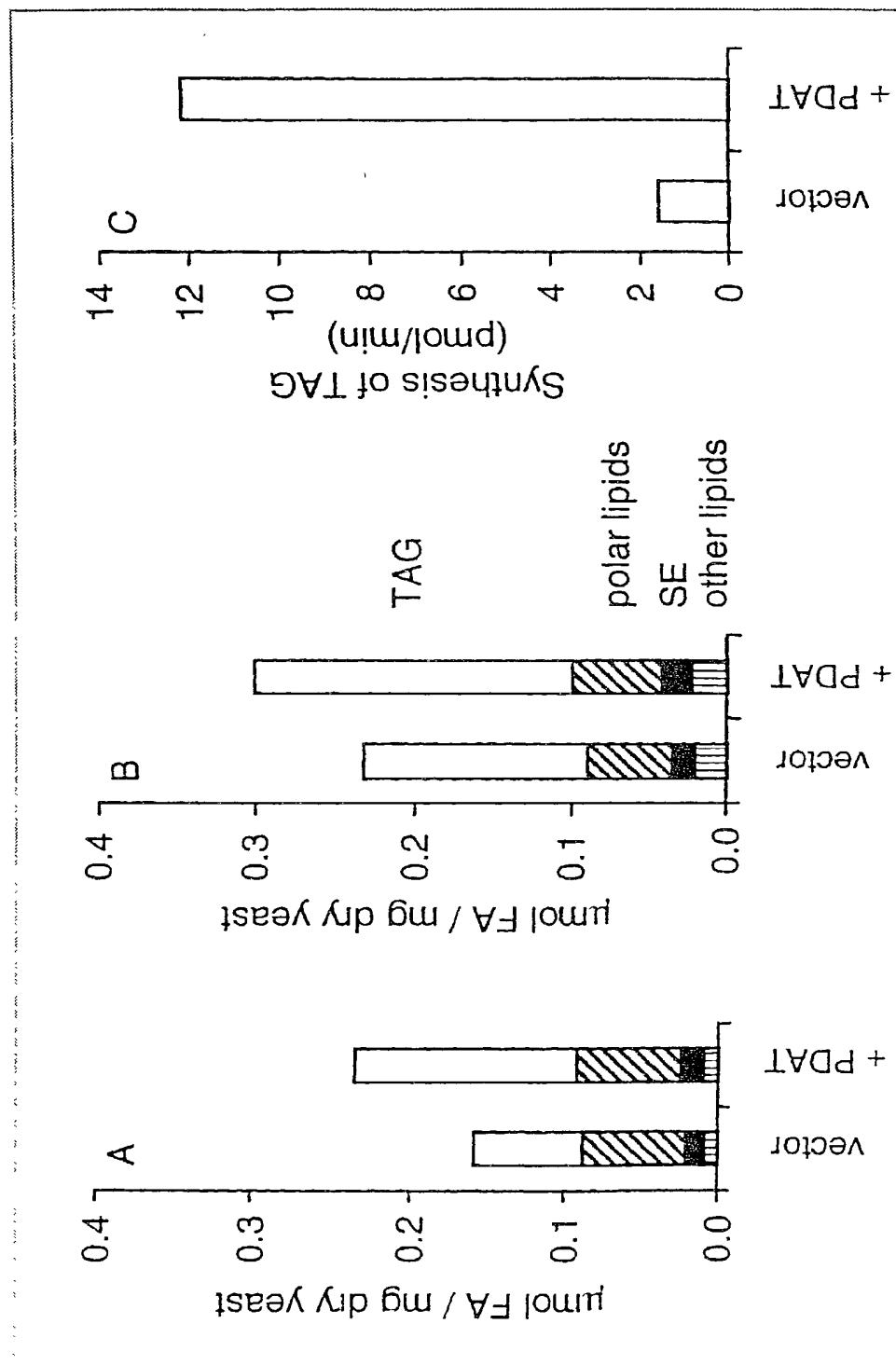
**Fig 2**

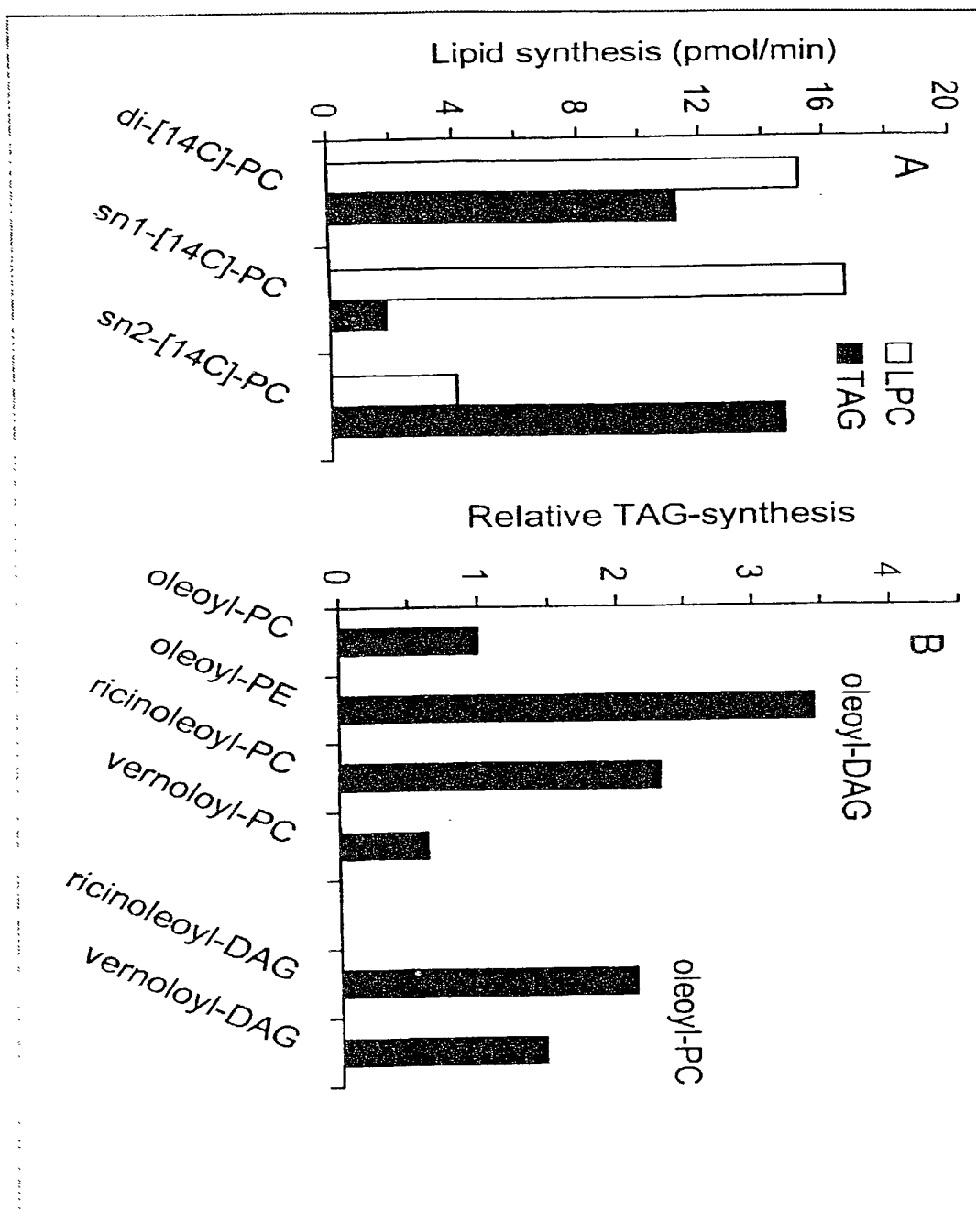
Fig 3:

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Fig.4:



## Tables

Tab. 1:

Substrate added [ $^{14}\text{C}$ ]-lipid <sup>(2)</sup>	mol % of added [ $^{14}\text{C}$ ]-acyl group in TAG <sup>(1)</sup>					
	1-OH-TAG	2-OH-TAG	1-OH-1-ver-TAG	1-OH-2-ver-TAG	3-OH-TAG	
unlabelled lipid <sup>(2)</sup>						
A mono-[ $^{14}\text{C}$ ]-ricinoleoyl-DAG	2,8	12,4	-	-	-	
A mono-[ $^{14}\text{C}$ ]-ricinoleoyl-DAG	3,2	12,1	1,3	-	-	
A mono-[ $^{14}\text{C}$ ]-ricinoleoyl-DAG	4	10	0,5	1,2	-	
A mono-[ $^{14}\text{C}$ ]-ricinoleoyl-DAG	0,3	24,8	-	-	-	
B mono-[ $^{14}\text{C}$ ]-ricinoleoyl-PC	6,8	8,0	-	-	4,7	
C mono-[ $^{14}\text{C}$ ]-ricinoleoyl-PC	8,6	9,8	-	-	5,0	
C mono-[ $^{14}\text{C}$ ]-ricinoleoyl-PC	5,7	16,7	-	-	1,9	
C mono-[ $^{14}\text{C}$ ]-ricinoleoyl-PC	4,5	9,4	-	-	9,5	
C mono-[ $^{14}\text{C}$ ]-ricinoleoyl-PC	6,0	11,5	10,9	0,5	7,4	
C mono-[ $^{14}\text{C}$ ]-ricinoleoyl-PC	6,7	10,8	1,1	8,4	6,8	

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Tab. 2:

T1 plant	T2 plant number	nmol fatty acids per mg seed		standard deviation
32-4	1	1277		$\pm 11$ (n=2)
	4	1261		$\pm 63$ (n=3)
	5	1369		$\pm 17$ (n=3)
	6	1312		$\pm 53$ (n=4)
	7	1197		$\pm 54$ (n=5)
	8	1240		$\pm 78$ (n=4)
	9	1283		$\pm 54$ (n=5)
	10	1381		$\pm 35$ (n=5)
26-14	1	1444		$\pm 110$ (n=4)
	2	1617*		$\pm 109$ (n=4)
	3	1374		$\pm 37$ (n=2)
	5	1562*		$\pm 70$ (n=4)
	6	1393		$\pm 77$ (n=4)
	7	1433		$\pm 98$ (n=4)
	8	1581*		$\pm 82$ (n=4)

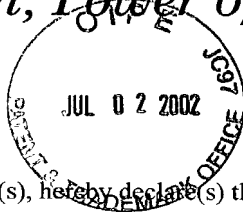


# Declaration, Power of Attorney and Petition



26474

PATENT & TRADEMARK OFFICE



Page 1 of 4  
0093/000003

We (I), the undersigned inventor(s), hereby declare(s) that:

My residence, post office address and citizenship are as stated below next to my name,

We (I) believe that we are (I am) the original, first, and joint (sole) inventor(s) of the subject matter which is claimed and for which a patent is sought on the invention entitled

NEW CLASS OF ENZYMES IN THE BIOSYNTHETIC PATHWAY FOR THE PRODUCTION OF  
TRIACYCLOGLYCEROL AND RECOMBINANT DNA MOLECULES ENCODING THESE ENZYMES

the specification of which

☐ is attached hereto.

☒ was filed on September 28, 2001 as

Application Serial No. 09/937,779

and amended on \_\_\_\_\_.

☒ was filed as PCT international application

Number PCT/EP/00/02701

on March 28, 2000

and was amended under PCT Article 19

on \_\_\_\_\_ (if applicable).

We (I) hereby state that we (I) have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

We (I) acknowledge the duty to disclose information known to be material to the patentability of this application as defined in Section 1.56 of Title 37 Code of Federal Regulations.

We (I) hereby claim foreign priority benefits under 35 U.S.C. § 119(a)–(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed. Prior Foreign Application(s)

Application No.	Country	Day/Month/Year	Priority Claimed
99106656.4	Europe	01 April 1999	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No
99111321.8	Europe	10 June 1999	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No
60/180687	United States of America	07 February 2000	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No

0093/000003

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0093/000003

(Filing Date)

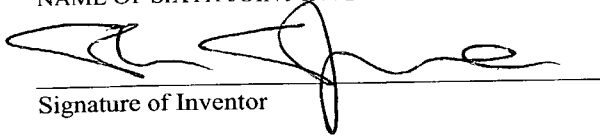
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**Application Serial No.**

**Status (pending, patented,  
abandoned)**


We (I) declare that all statements made herein of our (my) own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

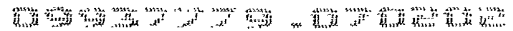
6-w  
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SEX



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16

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19

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<213> Arabidopsis thaliana

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Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met  
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Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly  
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Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr  
115 120 125

Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val  
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	210					215					220				
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225					230					235					240
Phe	Thr	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ser	Thr	Asp	Tyr	Phe	Ile
				245					250					255	
Ala	Gly	Tyr	Trp	Ile	Trp	Asn	Lys	Val	Phe	Gln	Asn	Leu	Gly	Val	Ile
			260					265					270		
Gly	Tyr	Glu	Pro	Asn	Lys	Met	Thr	Ser	Ala	Ala	Tyr	Asp	Trp	Arg	Leu
		275					280					285			
Ala	Tyr	Leu	Asp	Leu	Glu	Arg	Arg	Asp	Arg	Tyr	Phe	Thr	Lys	Leu	Lys
	290					295					300				
Glu	Gln	Ile	Glu	Leu	Phe	His	Gln	Leu	Ser	Gly	Glu	Lys	Val	Cys	Leu
305					310					315					320
Ile	Gly	His	Ser	Met	Gly	Ser	Gln	Ile	Ile	Phe	Tyr	Phe	Met	Lys	Trp
				325					330					335	
Val	Glu	Ala	Glu	Gly	Pro	Leu	Tyr	Gly	Asn	Gly	Gly	Arg	Gly	Trp	Val
			340					345					350		
Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly
		355					360					365			
Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr
	370					375					380				
Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser
385					390					395					400
Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser
				405					410					415	
Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser

420	425	430
Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile		
435	440	445
Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met		
450	455	460
Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln		
465	470	475
Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu		
485	490	495
Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met		
500	505	510
Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr		
515	520	525
Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp		
530	535	540
Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro		
545	550	555
Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser		
565	570	575
Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly		
580	585	590
Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp		
595	600	605
Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser		
610	615	620
Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp		
625	630	635
Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln		
645	650	655
Met Pro Phe Pro Met		
660		

<210> 17  
 <211> 387  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 17

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1 5 10 15
Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val





Leu 1	Lys	Lys	Glu	Gly 5	Leu	Lys	Ala	Lys	His 10	Pro	Val	Val	Phe	Ile 15	Pro
Gly	Ile	Val	Thr 20	Gly	Gly	Leu	Glu	Leu 25	Trp	Glu	Gly	Lys	Gln 30	Cys	Ala
Asp	Gly	Leu 35	Phe	Arg	Lys	Arg	Leu 40	Trp	Gly	Gly	Thr	Phe 45	Leu	Cys	Trp
Val	Glu 50	His	Met	Ser	Leu	Asp 55	Asn	Glu	Thr	Gly	Leu 60	Asp	Pro	Ala	Gly
Ile 65	Arg	Val	Arg	Ala	Val 70	Ser	Gly	Leu	Val	Ala 75	Ala	Asp	Tyr	Phe	Ala 80
Pro	Gly	Tyr	Phe	Val 85	Trp	Ala	Val	Leu	Ile 90	Ala	Asn	Leu	Ala	His 95	Ile
Gly	Tyr	Glu	Glu 100	Lys	Asn	Met	Tyr	Met 105	Ala	Ala	Tyr	Asp	Trp 110	Arg	Leu
Ser	Phe	Gln 115	Asn	Thr	Glu	Arg	Asp 120	Gln	Thr	Leu	Ser	Arg 125	Met	Lys	Ser
Asn	Ile 130	Glu	Leu	Met	Val	Ser 135	Thr	Asn	Gly	Gly	Lys 140	Lys	Ala	Val	Ile
Val 145	Pro	His	Ser	Met	Gly 150	Val	Leu	Tyr	Phe	Leu 155	His	Phe	Met	Lys	Trp 160
Val	Glu	Ala	Pro	Ala 165	Pro	Leu	Gly	Gly	Gly 170	Gly	Gly	Pro	Asp	Trp 175	Cys
Ala	Lys	Tyr	Ile 180	Lys	Ala	Val	Met	Asn 185	Ile	Gly	Gly	Pro	Phe 190	Leu	Gly
Val	Pro	Lys 195	Ala	Val	Ala	Gly	Leu 200	Phe	Ser	Ala	Glu	Ala 205	Lys	Asp	Met

31

20	25	30	
aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly			144
35	40	45	
att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg			192
50	55	60	
aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu			240
65	70	75	80
att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe			288
85	90	95	
ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe			336
100	105	110	
gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val			384
115	120	125	
ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn			432
130	135	140	
tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly			480
145	150	155	160
aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val			528
165	170	175	
atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile			576
180	185	190	
gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp			624
195	200	205	
gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp			672
210	215	220	
ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn			720
225	230	235	240
ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile			768
245	250	255	



275	280	285	
gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag			912
Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys			
290	295	300	
gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta			960
Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu			
305	310	315	320
att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg			1008
Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp			
	325	330	335
gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt			1056
Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val			
	340	345	350
aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc			1104
Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly			
	355	360	365
gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc			1152
Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr			
	370	375	380
att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca			1200
Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser			
	385	390	395
aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca			1248
Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser			
	405	410	415
atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct			1296
Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser			
	420	425	430
tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att			1344
Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile			
	435	440	445
cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg			1392
Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met			
	450	455	460
aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa			1440
Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln			
	465	470	475
aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa			1488
Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu			
	485	490	495
gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg			1536
Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met			
	500	505	510
gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac			1584

34

Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr		
		515					520					525					
ggg	gtg	aac	aac	cca	act	gaa	agg	gca	tat	gta	tat	aag	gaa	gag	gat	1632	
Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp		
	530					535				540							
gac	tcc	tct	gct	ctg	aat	ttg	acc	atc	gac	tac	gaa	agc	aag	caa	cct	1680	
Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro		
545					550				555						560		
gta	ttc	ctc	acc	gag	ggg	gac	gga	acc	gtt	ccg	ctc	gtg	gcg	cat	tca	1728	
Val	Phe	Leu	Thr	Glu	Gly	Asp	Gly	Thr	Val	Pro	Leu	Val	Ala	His	Ser		
				565					570					575			
atg	tgt	cac	aaa	tgg	gcc	cag	ggg	gct	tca	ccg	tac	aac	cct	gcc	gga	1776	
Met	Cys	His	Lys	Trp	Ala	Gln	Gly	Ala	Ser	Pro	Tyr	Asn	Pro	Ala	Gly		
			580					585					590				
att	aac	gtt	act	att	gtg	gaa	atg	aaa	cac	cag	cca	gat	cga	ttt	gat	1824	
Ile	Asn	Val	Thr	Ile	Val	Glu	Met	Lys	His	Gln	Pro	Asp	Arg	Phe	Asp		
	595						600					605					
ata	cgt	ggg	gga	gca	aaa	agc	gcc	gaa	cac	gta	gac	atc	ctc	ggc	agc	1872	
Ile	Arg	Gly	Gly	Ala	Lys	Ser	Ala	Glu	His	Val	Asp	Ile	Leu	Gly	Ser		
	610					615					620						
gcg	gag	ttg	aac	gat	tac	atc	ttg	aaa	att	gca	agc	ggg	aat	ggc	gat	1920	
Ala	Glu	Leu	Asn	Asp	Tyr	Ile	Leu	Lys	Ile	Ala	Ser	Gly	Asn	Gly	Asp		
625						630				635					640		
ctc	gtc	gag	cca	cgc	caa	ttg	tct	aat	ttg	agc	cag	tgg	gtt	tct	cag	1968	
Leu	Val	Glu	Pro	Arg	Gln	Leu	Ser	Asn	Leu	Ser	Gln	Trp	Val	Ser	Gln		
				645					650					655			
atg	ccc	ttc	cca	atg	taa											1986	
Met	Pro	Phe	Pro	Met													
			660														

<210> 20  
 <211> 661  
 <212> PRT  
 <213> Saccharomyces cerevisiae

<400> 20

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		20						25					30				
Asn	His	Ile	His	His	Gln	Gln	Gly	Leu	Gly	His	Lys	Arg	Arg	Arg	Gly		
		35					40					45					
Ile	Ser	Gly	Ser	Ala	Lys	Arg	Asn	Glu	Arg	Gly	Lys	Asp	Phe	Asp	Arg		
	50					55					60						

Lys 65	Arg	Asp	Gly	Asn	Gly 70	Arg	Lys	Arg	Trp	Arg 75	Asp	Ser	Arg	Arg	Leu 80
Ile	Phe	Ile	Leu	Gly 85	Ala	Phe	Leu	Gly	Val 90	Leu	Leu	Pro	Phe	Ser 95	Phe
Gly	Ala	Tyr	His 100	Val	His	Asn	Ser	Asp 105	Ser	Asp	Leu	Phe	Asp 110	Asn	Phe
Val	Asn	Phe 115	Asp	Ser	Leu	Lys	Val 120	Tyr	Leu	Asp	Asp	Trp 125	Lys	Asp	Val
Leu	Pro 130	Gln	Gly	Ile	Ser	Ser 135	Phe	Ile	Asp	Asp	Ile 140	Gln	Ala	Gly	Asn
Tyr 145	Ser	Thr	Ser	Ser	Leu 150	Asp	Asp	Leu	Ser	Glu 155	Asn	Phe	Ala	Val	Gly 160
Lys	Gln	Leu	Leu	Arg 165	Asp	Tyr	Asn	Ile	Glu 170	Ala	Lys	His	Pro	Val 175	Val
Met	Val	Pro	Gly 180	Val	Ile	Ser	Thr	Gly 185	Ile	Glu	Ser	Trp	Gly 190	Val	Ile
Gly	Asp	Asp 195	Glu	Cys	Asp	Ser	Ser 200	Ala	His	Phe	Arg	Lys 205	Arg	Leu	Trp
Gly	Ser 210	Phe	Tyr	Met	Leu	Arg 215	Thr	Met	Val	Met	Asp 220	Lys	Val	Cys	Trp
Leu 225	Lys	His	Val	Met	Leu 230	Asp	Pro	Glu	Thr	Gly 235	Leu	Asp	Pro	Pro	Asn 240
Phe	Thr	Leu	Arg	Ala 245	Ala	Gln	Gly	Phe	Glu 250	Ser	Thr	Asp	Tyr	Phe 255	Ile
Ala	Gly	Tyr	Trp 260	Ile	Trp	Asn	Lys	Val	Phe	Gln	Asn	Leu	Gly 270	Val	Ile
Gly	Tyr	Glu 275	Pro	Asn	Lys	Met	Thr 280	Ser	Ala	Ala	Tyr	Asp 285	Trp	Arg	Leu
Ala	Tyr 290	Leu	Asp	Leu	Glu	Arg 295	Arg	Asp	Arg	Tyr	Phe 300	Thr	Lys	Leu	Lys
Glu 305	Gln	Ile	Glu	Leu	Phe 310	His	Gln	Leu	Ser	Gly 315	Glu	Lys	Val	Cys	Leu 320
Ile	Gly	His	Ser	Met 325	Gly	Ser	Gln	Ile	Ile 330	Phe	Tyr	Phe	Met	Lys 335	Trp
Val	Glu	Ala	Glu 340	Gly	Pro	Leu	Tyr	Gly 345	Asn	Gly	Gly	Arg	Gly 350	Trp	Val
Asn	Glu	His 355	Ile	Asp	Ser	Phe	Ile 360	Asn	Ala	Ala	Gly	Thr 365	Leu	Leu	Gly
Ala	Pro 370	Lys	Ala	Val	Pro	Ala 375	Leu	Ile	Ser	Gly	Glu 380	Met	Lys	Asp	Thr

<210> 21  
<211> 1986



37

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gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg	624
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp	
195 200 205	
gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg	672
Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp	
210 215 220	
ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac	720
Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn	
225 230 235 240	
ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc	768
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile	
245 250 255	
gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att	816
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile	
260 265 270	
ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt	864
Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu	
275 280 285	
gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag	912
Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys	
290 295 300	
gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta	960
Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu	
305 310 315 320	
att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg	1008
Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp	
325 330 335	
gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt	1056
Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val	
340 345 350	
aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc	1104
Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly	
355 360 365	
gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc	1152
Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr	
370 375 380	
att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca	1200
Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser	
385 390 395 400	
aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca	1248
Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser	
405 410 415	

Gly	Asp	Asp	Glu	Cys	Asp	Ser	Ser	Ala	His	Phe	Arg	Lys	Arg	Leu	Trp		
			195					200					205				
gga	agt	ttt	tac	atg	ctg	aga	aca	atg	gtt	atg	gat	aaa	gtt	tgt	tgg	672	
Gly	Ser	Phe	Tyr	Met	Leu	Arg	Thr	Met	Val	Met	Asp	Lys	Val	Cys	Trp		
		210					215				220						
ttg	aaa	cat	gta	atg	tta	gat	cct	gaa	aca	ggg	ctg	gac	cca	ccg	aac	720	
Leu	Lys	His	Val	Met	Leu	Asp	Pro	Glu	Thr	Gly	Leu	Asp	Pro	Pro	Asn		240
	225					230					235						
ttt	acg	cta	cgt	gca	gca	cag	ggc	ttc	gaa	tca	act	gat	tat	ttc	atc	768	
Phe	Thr	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ser	Thr	Asp	Tyr	Phe	Ile		
				245					250					255			
gca	ggg	tat	tgg	att	tgg	aac	aaa	gtt	ttc	caa	aat	ctg	gga	gta	att	816	
Ala	Gly	Tyr	Trp	Ile	Trp	Asn	Lys	Val	Phe	Gln	Asn	Leu	Gly	Val	Ile		
			260					265						270			
ggc	tat	gaa	ccc	aat	aaa	atg	acg	agt	gct	gcg	tat	gat	tgg	agg	ctt	864	
Gly	Tyr	Glu	Pro	Asn	Lys	Met	Thr	Ser	Ala	Ala	Tyr	Asp	Trp	Arg	Leu		
		275				280						285					
gca	tat	tta	gat	cta	gaa	aga	cgc	gat	agg	tac	ttt	acg	aag	cta	aag	912	
Ala	Tyr	Leu	Asp	Leu	Glu	Arg	Arg	Asp	Arg	Tyr	Phe	Thr	Lys	Leu	Lys		
		290				295					300						
gaa	caa	atc	gaa	ctg	ttt	cat	caa	ttg	agt	ggg	gaa	aaa	gtt	tgt	tta	960	
Glu	Gln	Ile	Glu	Leu	Phe	His	Gln	Leu	Ser	Gly	Glu	Lys	Val	Cys	Leu		
	305				310					315					320		
att	gga	cat	tct	atg	ggg	tct	cag	att	atc	ttt	tac	ttt	atg	aaa	tgg	1008	
Ile	Gly	His	Ser	Met	Gly	Ser	Gln	Ile	Ile	Phe	Tyr	Phe	Met	Lys	Trp		
			325					330						335			
gtc	gag	gct	gaa	ggc	cct	ctt	tac	ggg	aat	ggg	ggg	cgt	ggc	tgg	gtt	1056	
Val	Glu	Ala	Glu	Gly	Pro	Leu	Tyr	Gly	Asn	Gly	Gly	Arg	Gly	Trp	Val		
			340					345					350				
aac	gaa	cac	ata	gat	tca	ttc	att	aat	gca	gca	ggg	acg	ctt	ctg	ggc	1104	
Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly		
		355				360						365					
gct	cca	aag	gca	gtt	cca	gct	cta	att	agt	ggg	gaa	atg	aaa	gat	acc	1152	
Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr		
		370				375					380						
att	caa	tta	aat	acg	tta	gcc	atg	tat	ggg	ttg	gaa	aag	ttc	ttc	tca	1200	
Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser		
		385			390					395					400		
aga	att	gag	aga	gta	aaa	atg	tta	caa	acg	tgg	ggg	ggg	ata	cca	tca	1248	
Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser		
			405					410						415			
atg	cta	cca	aag	gga	gaa	gag	gtc	att	tgg	ggg	gat	atg	aag	tca	tct	1296	
Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser		
			420				425						430				

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Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln	
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Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp	
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 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 22

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Asn	His	Ile	His	His	Gln	Gln	Gly	Leu	Gly	His	Lys	Arg	Arg	Arg	Gly	35	40	45	
Ile	Ser	Gly	Ser	Ala	Lys	Arg	Asn	Glu	Arg	Gly	Lys	Asp	Phe	Asp	Arg	50	55	60	
Lys	Arg	Asp	Gly	Asn	Gly	Arg	Lys	Arg	Trp	Arg	Asp	Ser	Arg	Arg	Leu	65	70	75	80
Ile	Phe	Ile	Leu	Gly	Ala	Phe	Leu	Gly	Val	Leu	Leu	Pro	Phe	Ser	Phe	85	90	95	
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Leu	Lys	His	Val	Met	Leu	Asp	Pro	Glu	Thr	Gly	Leu	Asp	Pro	Pro	Asn	225	230	235	240
Phe	Thr	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ser	Thr	Asp	Tyr	Phe	Ile	245	250	255	
Ala	Gly	Tyr	Trp	Ile	Trp	Asn	Lys	Val	Phe	Gln	Asn	Leu	Gly	Val	Ile	260	265	270	

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43

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atg ccc ctt att cat cgg aaa aag ccg acg gag aaa cca tcg acg ccg 167
Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro
  1             5             10             15
cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac 215
Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His
          20             25             30
gaa tct tcc aaa tcc cac cat aag naa tcg aac gga gga ggg aag tgg 263
Glu Ser Ser Lys Ser His His Lys Xaa Ser Asn Gly Gly Gly Lys Trp
          35             40             45
tcg tgc atc gat tct tgt tgt tgg ttc att ggg tgt gtg tgt gta acc 311
Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
          50             55             60
tgg tgg ttt ctt ctc ttc ctt tac aac gca atg cct gcg agc ttc cct 359
Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
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 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly  
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 35 40 45  
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 35 40 45

48

Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly  
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 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile  
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 <212> DNA  
 <213> *Arabidopsis thaliana*

<400> 29

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50

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09/937779

JC05 Rec'd PCT/PTO 2 8 SEP 2001

## SEQUENCE LISTENING

&lt;110&gt; BASF AG

<120> A NEW CLASS OF ENZYMES IN THE BIOSYNTHETIC PATHWAY FOR  
THE PRODUCTION OF TRIACYLGLYCEROL AND RECOMBINANT DNA  
MOLECULES ENCODING THESE ENZYMES

&lt;130&gt; BASF-NAE-3377-99-Sept-2000

&lt;140&gt; PCT/EP 00/02701

&lt;141&gt; 2000-03-23

&lt;160&gt; 31

&lt;170&gt; PatentIn Ver. 2.1

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&lt;221&gt; CDS

&lt;222&gt; (1)..(1983)

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ttaacattga aattctctcc actagcgtt agactctgta tatgcaactg taacactaac 2040  
aaaagtcca ccaagaatgt tcactcccat atttcgttcc ttgatgtgt atccatcagt 2100  
tacagaaaca gctctagtca acatgaccag catggaatgt ggcttccca ccttttctc 2160  
ttcacagcc cgtgaactag cagatgggac ttttttcaaa gcaatagaag acctatgacc 2220  
agatagcaag aggatgttac accagctaaa gaagtacgta ccttctcttg tgataagaaa 2280  
tattgtctat cgatcatcac ttgctggctt cttgtacgtc aaattgtttt gttcaaatct 2340  
ctatcatcat tgttcatatg ctttgtctt ctactataa gaaacaagta taatcagaaa 2400  
ccttatttat gattatcagt tctctcttta tattatggaa tgccttttct gtttacagt 2460  
atgaatgcaa aaggggtgat tttagtcgat tgattctctc attctctagt ttgttttgac 2520  
taatagcgtc aattttgttt tcttagcaaa tcttgtgaa ttatatataa catgctaact 2580  
atacttttca ggttgatca tgatgacct gcttttaact ccttgactcc ttgggagaga 2640  
ccacctataa aaaatgtatt ttgcatacat ggtgctcatc taagacaga ggtatgatgc 2700  
attctcaata tcacattatg cgttgacttt gttattatat ccccatctg gtttgcaata 2760  
cttttttgaa ttatgattta tcttctccct tgcattctat gctatgaagc gttaaaggta 2820  
ctaaatgtat gaagcgtct gtcataggtt ggttattact ttgccccaa tgccaaacct 2880  
tactctgata attggaatc caccgatatc atttatgaaa ctgaaggctc cctcgtgtca 2940  
aggtaattt ccgcaatggc agaagtaaaa cagggaaggc aagctctctg tatcagttca 3000  
gtggcatgtt atctcagttg cataagcaaa ttattaaaca actaaaattt aagtactctt 3060  
ctatcatccc ttttgagct agtggatgat cagtggctta aagtggaag aggtgttgca 3120  
tgaaacatga cacttgatc aaagataact agcaaaacaa aactaaccca tttctgaatt 3180

tcatattatt aggagtagtc gtgcttttaa aaaatttgtt ttaagaaacc gaaaaactag 3240  
ttcataatctt gattgtgcaa tatctgcagg tctggaactg tggttgatgg gaacgctgga 3300  
cctataactg gggatgagac ggtaagctca gaagtgtgtt ttgaaattat cttcttgcaa 3360  
actactgaag actaagataa tacttgcttc tggaaactg ctgctatgt tctctagtac 3420  
actgcaatat tgactctccg ctacttttat cgattatgaa attgatctct tataggtacc 3480  
ctatcattca ctctcttggg gcaagaattg gctcggacct aaagttaaca taacaatggc 3540  
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ctgggttatgt gttgatttac ctccaatttg ttctttctaa aaatcatata tctctgtact 3660  
cctcaagaac ttgtattaat ctaaacgaga ttctcattgg gaaaataaaa caacagccag 3720  
aacacgatgg aagcgacgta catgtggaac taaatgttga tcatgagcat gggtcagaca 3780  
tcatagctaa catgacaaaa gcaccaaggg ttaagtacat aaccttttat gaagactctg 3840  
agagcattec ggggaagaga accgcagctc gggagcttga taaaagtggg tattaa 3896

<210> 12  
<211> 709  
<212> cDNA  
<213> Lycopersicon esculentum

<400> 12  
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aagtgcacct aaatatagag catcaacatg gtgaagatat cattcccaat atgacaaagt 120  
tacctacaat gaagtacata acctattatg aggattctga aagttttcca gggacaagaa 180  
cagcagtttg ggagcttgat aaagcaaate acaggaacat tgtcagatct ccagctttga 240  
tgcgggagct gtggcttgag atgtggcatg atattcatcc tgataaaaag tccaagtttg 300  
ttacaaaagg tgggtgtctga tcttcactat tttcttctat aaatgtttga gtttgcattg 360  
acattgtaag tattgcaaca aaaagcaaag cgtgggcctc tgagggatga ggactgctat 420  
tgggattacg ggaaagctcg atgtgcatgg gctgaacatt gtgaatacag gttagaatat 480  
tcaaattata ttttgcaaaa tattctcttt ttgtgtattt aggccacctt tccccgggca 540  
caacgatgca gatatgtatt cggggatggt caccggggac agagttgcag attgaagagt 600  
tctacatctc acatcctgtc acactatgtg tgatatttaa gaaactttgt ttggcggaac 660  
aacaagtttg cacaacatt tgaagaagaa agcgaaatga ttcagagag 709

<210> 13  
<211> 623  
<212> PRT  
<213> Schizosaccharomyces pombe

<400> 13

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Lys Ser Pro Ile Asp Leu Pro Asn Ser Lys Lys Pro Thr Arg Ala Leu  
20 25 30  
Ser Glu Gln Pro Ser Ala Ser Glu Thr Gln Ser Val Ser Asn Lys Ser  
35 40 45  
Arg Lys Ser Lys Phe Gly Lys Arg Leu Asn Phe Ile Leu Gly Ala Ile  
50 55 60  
Leu Gly Ile Cys Gly Ala Phe Phe Phe Ala Val Gly Asp Asp Asn Ala  
65 70 75 80  
Val Phe Asp Pro Ala Thr Leu Asp Lys Phe Gly Asn Met Leu Gly Ser  
85 90 95  
Ser Asp Leu Phe Asp Asp Ile Lys Gly Tyr Leu Ser Tyr Asn Val Phe  
100 105 110  
Lys Asp Ala Pro Phe Thr Thr Asp Lys Pro Ser Gln Ser Pro Ser Gly  
115 120 125  
Asn Glu Val Gln Val Gly Leu Asp Met Tyr Asn Glu Gly Tyr Arg Ser  
130 135 140  
Asp His Pro Val Ile Met Val Pro Gly Val Ile Ser Ser Gly Leu Glu  
145 150 155 160  
Ser Trp Ser Phe Asn Asn Cys Ser Ile Pro Tyr Phe Arg Lys Arg Leu  
165 170 175  
Trp Gly Ser Trp Ser Met Leu Lys Ala Met Phe Leu Asp Lys Gln Cys  
180 185 190  
Trp Leu Glu His Leu Met Leu Asp Lys Lys Thr Gly Leu Asp Pro Lys  
195 200 205  
Gly Ile Lys Leu Arg Ala Ala Gln Gly Phe Glu Ala Ala Asp Phe Phe  
210 215 220  
Ile Thr Gly Tyr Trp Ile Trp Ser Lys Val Ile Glu Asn Leu Ala Ala  
225 230 235 240  
Ile Gly Tyr Glu Pro Asn Asn Met Leu Ser Ala Ser Tyr Asp Trp Arg  
245 250 255  
Leu Ser Tyr Ala Asn Leu Glu Glu Arg Asp Lys Tyr Phe Ser Lys Leu  
260 265 270

Lys Met Phe Ile Glu Tyr Ser Asn Ile Val His Lys Lys Lys Val Val  
275 280 285

Leu Ile Ser His Ser Met Gly Ser Gln Val Thr Tyr Tyr Phe Phe Lys  
290 295 300

Trp Val Glu Ala Glu Gly Tyr Gly Asn Gly Gly Pro Thr Trp Val Asn  
305 310 315 320

Asp His Ile Glu Ala Phe Ile Asn Ile Ser Gly Ser Leu Ile Gly Ala  
325 330 335

Pro Lys Thr Val Ala Ala Leu Leu Ser Gly Glu Met Lys Asp Thr Gly  
340 345 350

Ile Val Ile Thr Leu Asn Ile Leu Glu Lys Phe Phe Ser Arg Ser Glu  
355 360 365

Arg Ala Met Met Val Arg Thr Met Gly Gly Val Ser Ser Met Leu Pro  
370 375 380

Lys Gly Gly Asp Val Ala Pro Asp Asp Leu Asn Gln Thr Asn Phe Ser  
385 390 395 400

Asn Gly Ala Ile Ile Arg Tyr Arg Glu Asp Ile Asp Lys Asp His Asp  
405 410 415

Glu Phe Asp Ile Asp Asp Ala Leu Gln Phe Leu Lys Asn Val Thr Asp  
420 425 430

Asp Asp Phe Lys Val Met Leu Ala Lys Asn Tyr Ser His Gly Leu Ala  
435 440 445

Trp Thr Glu Lys Glu Val Leu Lys Asn Asn Glu Met Pro Ser Lys Trp  
450 455 460

Ile Asn Pro Leu Glu Thr Ser Leu Pro Tyr Ala Pro Asp Met Lys Ile  
465 470 475 480

Tyr Cys Val His Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Tyr Tyr  
485 490 495

Thr Asn Asn Pro Glu Gly Gln Pro Val Ile Asp Ser Ser Val Asn Asp  
500 505 510

Gly Thr Lys Val Glu Asn Gly Ile Val Met Asp Asp Gly Asp Gly Thr  
515 520 525

Leu Pro Ile Leu Ala Leu Gly Leu Val Cys Asn Lys Val Trp Gln Thr  
530 535 540

Lys Arg Phe Asn Pro Ala Asn Thr Ser Ile Thr Asn Tyr Glu Ile Lys  
545 550 555 560

His Glu Pro Ala Ala Phe Asp Leu Arg Gly Gly Pro Arg Ser Ala Glu  
565 570 575

His Val Asp Ile Leu Gly His Ser Glu Leu Asn Glu Ile Ile Leu Lys  
580 585 590

Val Ser Ser Gly His Gly Asp Ser Val Pro Asn Arg Tyr Ile Ser Asp  
595 600 605

Ile Gln Glu Ile Ile Asn Glu Ile Asn Leu Asp Lys Pro Arg Asn  
610 615 620



<210> 14  
<211> 432  
<212> PRT  
<213> Arabidopsis thaliana

<400> 14  
Met Lys Lys Ile Ser Ser His Tyr Ser Val Val Ile Ala Ile Leu Val  
1 5 10 15  
Val Val Thr Met Thr Ser Met Cys Gln Ala Val Gly Ser Asn Val Tyr  
20 25 30  
Pro Leu Ile Leu Val Pro Gly Asn Gly Gly Asn Gln Leu Glu Val Arg  
35 40 45  
Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val Trp Cys Ser Ser Trp Leu  
50 55 60  
Tyr Pro Ile His Lys Lys Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp  
65 70 75 80  
Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met  
85 90 95  
Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly  
100 105 110  
Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr  
115 120 125  
Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val  
130 135 140  
Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu  
145 150 155 160  
Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro  
165 170 175  
Ser Arg Val Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu  
180 185 190  
Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His  
195 200 205  
Ser Leu Gly Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro  
210 215 220  
Ser Trp Arg Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro  
225 230 235 240  
Trp Gly Gly Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr  
245 250 255  
Leu Gly Val Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg  
260 265 270  
Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His  
275 280 285

Asp	Arg	Thr	Lys	Pro	Leu	Val	Val	Thr	Pro	Gln	Val	Asn	Tyr	Thr	Ala
290						295					300				
Tyr	Glu	Met	Asp	Arg	Phe	Phe	Ala	Asp	Ile	Gly	Phe	Ser	Gln	Gly	Val
305					310					315					320
Val	Pro	Tyr	Lys	Thr	Arg	Val	Leu	Pro	Leu	Thr	Glu	Glu	Leu	Met	Thr
				325						330				335	
Pro	Gly	Val	Pro	Val	Thr	Cys	Ile	Tyr	Gly	Arg	Gly	Val	Asp	Thr	Pro
			340						345				350		
Glu	Val	Leu	Met	Tyr	Gly	Lys	Gly	Gly	Phe	Asp	Lys	Gln	Pro	Glu	Ile
		355					360					365			
Lys	Tyr	Gly	Asp	Gly	Asp	Gly	Thr	Val	Asn	Leu	Ala	Ser	Leu	Ala	Ala
	370					375					380				
Leu	Lys	Val	Asp	Ser	Leu	Asn	Thr	Val	Glu	Ile	Asp	Gly	Val	Ser	His
385					390					395					400
Thr	Ser	Ile	Leu	Lys	Asp	Glu	Ile	Ala	Leu	Lys	Glu	Ile	Met	Lys	Gln
				405						410				415	
Ile	Ser	Ile	Ile	Asn	Tyr	Glu	Leu	Ala	Asn	Val	Asn	Ala	Val	Asn	Glu
			420					425					430		

<210> 15  
<211> 552  
<212> PRT  
<213> Arabidopsis thaliana

<400> 15  
Met Gly Ala Asn Ser Lys Ser Val Thr Ala Ser Phe Thr Val Ile Ala  
1 5 10 15  
Val Phe Phe Leu Ile Cys Gly Gly Arg Thr Ala Val Glu Asp Glu Thr  
20 25 30  
Glu Phe His Gly Asp Tyr Ser Lys Leu Ser Gly Ile Ile Ile Pro Gly  
35 40 45  
Phe Ala Ser Thr Gln Leu Arg Ala Trp Ser Ile Leu Asp Cys Pro Tyr  
50 55 60  
Thr Pro Leu Asp Phe Asn Pro Leu Asp Leu Val Trp Leu Asp Thr Thr  
65 70 75 80  
Lys Leu Leu Ser Ala Val Asn Cys Trp Phe Lys Cys Met Val Leu Asp  
85 90 95  
Pro Tyr Asn Gln Thr Asp His Pro Glu Cys Lys Ser Arg Pro Asp Ser  
100 105 110  
Gly Leu Ser Ala Ile Thr Glu Leu Asp Pro Gly Tyr Ile Thr Gly Pro  
115 120 125  
Leu Ser Thr Val Trp Lys Glu Trp Leu Lys Trp Cys Val Glu Phe Gly  
130 135 140  
Ile Glu Ala Asn Ala Ile Val Ala Val Pro Tyr Asp Trp Arg Leu Ser  
145 150 155 160  
Pro Thr Lys Leu Glu Glu Arg Asp Leu Tyr Phe His Lys Leu Lys Leu  
165 170 175  
Thr Phe Glu Thr Ala Leu Lys Leu Arg Gly Gly Pro Ser Ile Val Phe  
180 185 190  
Ala His Ser Met Gly Asn Asn Val Phe Arg Tyr Phe Leu Glu Trp Leu  
195 200 205  
Arg Leu Glu Ile Ala Pro Lys His Tyr Leu Lys Trp Leu Asp Gln His  
210 215 220  
Ile His Ala Tyr Phe Ala Val Gly Ala Pro Leu Leu Gly Ser Val Glu  
225 230 235 240  
Ala Ile Lys Ser Thr Leu Ser Gly Val Thr Phe Gly Leu Pro Val Ser  
245 250 255  
Glu Gly Thr Ala Arg Leu Leu Ser Asn Ser Phe Ala Ser Ser Leu Trp  
260 265 270  
Leu Met Pro Phe Ser Lys Asn Cys Lys Gly Asp Asn Thr Phe Trp Thr  
275 280 285

His Phe Ser Gly Gly Ala Ala Lys Lys Asp Lys Arg Val Tyr His Cys  
290 295 300

Asp Glu Glu Glu Tyr Gln Ser Lys Tyr Ser Gly Trp Pro Thr Asn Ile  
305 310 315 320

Ile Asn Ile Glu Ile Pro Ser Thr Ser Ala Arg Glu Leu Ala Asp Gly  
325 330 335

Thr Leu Phe Lys Ala Ile Glu Asp Tyr Asp Pro Asp Ser Lys Arg Met  
340 345 350

Leu His Gln Leu Lys Lys Tyr Val Pro Phe Phe Val Ile Arg Asn Ile  
355 360 365

Ala His Arg Ser Ser Leu Ala Gly Phe Leu Leu Tyr His Asp Asp Pro  
370 375 380

Val Phe Asn Pro Leu Thr Pro Trp Glu Arg Pro Pro Ile Lys Asn Val  
385 390 395 400

Phe Cys Ile Tyr Gly Ala His Leu Lys Thr Glu Val Gly Tyr Tyr Phe  
405 410 415

Ala Pro Ser Gly Lys Pro Tyr Pro Asp Asn Trp Ile Ile Thr Asp Ile  
420 425 430

Ile Tyr Glu Thr Glu Gly Ser Leu Val Ser Arg Ser Gly Thr Val Val  
435 440 445

Asp Gly Asn Ala Gly Pro Ile Thr Gly Asp Glu Thr Val Pro Tyr His  
450 455 460

Ser Leu Ser Trp Cys Lys Asn Trp Leu Gly Pro Lys Val Asn Ile Thr  
465 470 475 480

Met Ala Pro Gln Ile Leu Ile Gly Lys Ile Lys Gln Gln Pro Glu His  
485 490 495

Asp Gly Ser Asp Val His Val Glu Leu Asn Val Asp His Glu His Gly  
500 505 510

Ser Asp Ile Ile Ala Asn Met Thr Lys Ala Pro Arg Val Lys Tyr Ile  
515 520 525

Thr Phe Tyr Glu Asp Ser Glu Ser Ile Pro Gly Lys Arg Thr Ala Val  
530 535 540

Trp Glu Leu Asp Lys Ser Gly Tyr  
545 550

<210> 16  
 <211> 661  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 16  
 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser  
     1                    5                    10                    15  
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg  
             20                    25                    30  
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly  
             35                    40                    45  
 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg  
     50                    55                    60  
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu  
     65                    70                    75                    80  
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe  
             85                    90                    95  
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe  
             100                    105                    110  
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val  
     115                    120                    125  
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn  
     130                    135                    140  
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly  
     145                    150                    155                    160  
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val  
             165                    170                    175  
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile  
             180                    185                    190  
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp  
             195                    200                    205  
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp  
     210                    215                    220  
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn  
     225                    230                    235                    240  
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile  
             245                    250                    255  
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile  
             260                    265                    270  
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu  
             275                    280                    285

Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys  
290 295 300

Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu  
305 310 315 320

Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp  
325 330 335

Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val  
340 345 350

Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly  
355 360 365

Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr  
370 375 380

Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser  
385 390 395 400

Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser  
405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser  
420 425 430

Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile  
435 440 445

Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met  
450 455 460

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln  
465 470 475 480

Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu  
485 490 495

Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met  
500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr  
515 520 525

Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp  
530 535 540

Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro  
545 550 555 560

Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser  
565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly  
580 585 590

Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp  
595 600 605

Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser  
610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp  
625 630 635 640

Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln  
645 650 655

Met Pro Phe Pro Met  
660

<210> 17  
<211> 387  
<212> PRT  
<213> Arabidopsis thaliana

<400> 17  
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Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val  
20 25 30  
Trp Cys Ser Ser Trp Leu Tyr Pro Ile His Lys Lys Ser Gly Gly Trp  
35 40 45  
Phe Arg Leu Trp Phe Asp Ala Ala Val Leu Leu Ser Pro Phe Thr Arg  
50 55 60  
Cys Phe Ser Asp Arg Met Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp  
65 70 75 80  
Tyr Gln Asn Ala Pro Gly Val Gln Thr Arg Val Pro His Phe Gly Ser  
85 90 95  
Thr Lys Ser Leu Leu Tyr Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser  
100 105 110  
Tyr Met Glu His Leu Val Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val  
115 120 125  
Asn Asp Gln Thr Ile Leu Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu  
130 135 140  
Ala Ala Ser Gly His Pro Ser Arg Val Ala Ser Gln Phe Leu Gln Asp  
145 150 155 160  
Leu Lys Gln Leu Val Glu Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro  
165 170 175  
Val Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu His Phe  
180 185 190  
Leu Asn Arg Thr Thr Pro Ser Trp Arg Arg Lys Tyr Ile Lys His Phe  
195 200 205  
Val Ala Leu Ala Ala Pro Trp Gly Gly Thr Ile Ser Gln Met Lys Thr  
210 215 220  
Phe Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val Asn Pro Leu Leu  
225 230 235 240  
Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro  
245 250 255  
Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu Val Val Thr Pro  
260 265 270  
Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile  
275 280 285



Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg Val Leu Pro Leu  
290 295 300

Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr Cys Ile Tyr Gly  
305 310 315 320

Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly Lys Gly Gly Phe  
325 330 335

Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn  
340 345 350

Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu Asn Thr Val Glu  
355 360 365

Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu  
370 375 380

Lys Glu Ile  
385

<210> 18  
<211> 389  
<212> PRT  
<213> Arabidopsis thaliana

<400> 18  
Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe Ile Pro  
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Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln Cys Ala  
20 25 30  
Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Leu Cys Trp  
35 40 45  
Val Glu His Met Ser Leu Asp Asn Glu Thr Gly Leu Asp Pro Ala Gly  
50 55 60  
Ile Arg Val Arg Ala Val Ser Gly Leu Val Ala Ala Asp Tyr Phe Ala  
65 70 75 80  
Pro Gly Tyr Phe Val Trp Ala Val Leu Ile Ala Asn Leu Ala His Ile  
85 90 95  
Gly Tyr Glu Glu Lys Asn Met Tyr Met Ala Ala Tyr Asp Trp Arg Leu  
100 105 110  
Ser Phe Gln Asn Thr Glu Arg Asp Gln Thr Leu Ser Arg Met Lys Ser  
115 120 125  
Asn Ile Glu Leu Met Val Ser Thr Asn Gly Gly Lys Lys Ala Val Ile  
130 135 140  
Val Pro His Ser Met Gly Val Leu Tyr Phe Leu His Phe Met Lys Trp  
145 150 155 160  
Val Glu Ala Pro Ala Pro Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys  
165 170 175  
Ala Lys Tyr Ile Lys Ala Val Met Asn Ile Gly Gly Pro Phe Leu Gly  
180 185 190  
Val Pro Lys Ala Val Ala Gly Leu Phe Ser Ala Glu Ala Lys Asp Met  
195 200 205  
Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu Pro Lys Gly  
210 215 220  
Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu Leu Pro Asn  
225 230 235 240  
Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile Pro Thr  
245 250 255  
Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser Cys Ile  
260 265 270  
Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp Ser Cys  
275 280 285

Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val Pro Val  
290 295 300

Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys Thr Arg  
305 310 315 320

Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn His Ser  
325 330 335

Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly Ala His  
340 345 350

Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met Arg Val  
355 360 365

Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val His Ser  
370 375 380

Gly Ile Phe Glu Trp  
385

<210> 19  
 <211> 1986  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
 <221> CDS  
 <222> (1)..(1983)

<400> 19  
 atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48  
 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser  
 1 5 10 15  
 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96  
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg  
 20 25 30  
 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144  
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly  
 35 40 45  
 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192  
 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg  
 50 55 60  
 aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240  
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu  
 65 70 75 80  
 att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288  
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe  
 85 90 95  
 ggc gct tat cat gtc cat aat agc gat agc gac ttg ttt gac aac ttt 336  
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe  
 100 105 110  
 gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gac gtt 384  
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val  
 115 120 125  
 ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac 432  
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn  
 130 135 140  
 tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt 480  
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly  
 145 150 155 160  
 aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta 528  
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val  
 165 170 175  
 atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att 576  
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile  
 180 185 190

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gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg 624
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
      195                200                205

gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg 672
Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
      210                215                220

ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac 720
Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
      225                230                235                240

ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc 768
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
      245                250                255

gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att 816
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
      260                265                270

ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt 864
Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
      275                280                285

gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag 912
Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
      290                295                300

gaa caa atc gaa ctg ttt cat caa tgc agt ggt gaa aaa gtt tgt cta 960
Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
      305                310                315                320

att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg 1008
Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
      325                330                335

gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt 1056
Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
      340                345                350

aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc 1104
Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
      355                360                365

gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc 1152
Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
      370                375                380

att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca 1200
Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
      385                390                395                400

aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca 1248
Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
      405                410                415

atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct 1296
Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
      420                425                430

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tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att 1344
Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
      435                      440                      445

cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg 1392
Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
      450                      455                      460

aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa 1440
Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
      465                      470                      475                      480

aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa 1488
Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
      485                      490                      495

gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg 1536
Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
      500                      505                      510

gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac 1584
Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
      515                      520                      525

ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat 1632
Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
      530                      535                      540

gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct 1680
Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
      545                      550                      555                      560

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca 1728
Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
      565                      570                      575

atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776
Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
      580                      585                      590

att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttc gat 1824
Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
      595                      600                      605

ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
      610                      615                      620

gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
      625                      630                      635                      640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtc tct cag 1968
Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
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atg ccc ttc cca arg taa 1986
Met Pro Phe Pro Met
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<212> PRT  
<213> *Saccharomyces cerevisiae*

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Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg  
20 25 30  
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly  
35 40 45  
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg  
50 55 60  
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu  
65 70 75 80  
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe  
85 90 95  
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe  
100 105 110  
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val  
115 120 125  
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn  
130 135 140  
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly  
145 150 155 160  
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val  
165 170 175  
Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile  
180 185 190  
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp  
195 200 205  
Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp  
210 215 220  
Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn  
225 230 235 240  
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile  
245 250 255  
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile  
260 265 270  
Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu  
275 280 285

Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys  
290 295 300

Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu  
305 310 315 320

Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp  
325 330 335

Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val  
340 345 350

Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly  
355 360 365

Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr  
370 375 380

Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser  
385 390 395 400

Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser  
405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser  
420 425 430

Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile  
435 440 445

Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met  
450 455 460

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln  
465 470 475 480

Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu  
485 490 495

Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met  
500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr  
515 520 525

Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp  
530 535 540

Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro  
545 550 555 560

Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser  
565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly  
580 585 590

Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp  
595 600 605



Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser  
610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp  
625 630 635 640

Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln  
645 650 655

Met Pro Phe Pro Met  
660

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 <211> 1986  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

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 <222> (1)..(1983)

<400> 21  
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 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser  
   1                  5                  10                  15  
 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96  
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg  
                   20                  25                  30  
 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144  
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly  
           35                  40                  45  
 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192  
 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg  
   50                  55                  60  
 aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240  
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu  
   65                  70                  75                  80  
 att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288  
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe  
           85                  90                  95  
 ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt 336  
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe  
          100                 105                 110  
 gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt 384  
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val  
          115                 120                 125  
 ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac 432  
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn  
          130                 135                 140  
 tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt 480  
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly  
  145                 150                 155                 160  
 aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta 528  
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val  
          165                 170                 175  
 atg gtc cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att 576  
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile  
          180                 185                 190

gga Gly	gac Asp	gat Asp 195	gag Glu	tgc Cys	gat Asp	agt Ser	tct Ser 200	gcg Ala	cat His	ttt Phe	cgt Arg	aaa Lys 205	cgg Arg	ctg Leu	tgg Trp	624
gga Gly	agt Ser 210	ttt Phe	tac Tyr	atg Met	ctg Leu	aga Arg 215	aca Thr	atg Met	gtt Val	atg Met 220	gat Asp	aaa Lys	gtt Val	tgt Cys	tgg Trp	672
ttg Leu 225	aaa Lys	cat His	gta Val	atg Met 230	tta Leu	gat Asp	cct Pro	gaa Glu	aca Thr	ggg Gly 235	ctg Leu	gac Asp	cca Pro	ccg Pro	aac Asn 240	720
ttt Phe	acg Thr	cta Leu	cgt Arg	gca Ala 245	gca Ala	cag Gln	ggc Gly	ttc Phe	gaa Glu 250	tca Ser	act Thr	gat Asp	tat Tyr	ttc Phe 255	atc Ile	768
gca Ala	ggg Gly	tat Tyr 260	tgg Trp	att Ile	tgg Trp	aac Asn	aaa Lys 265	gtt Val	ttc Phe	caa Gln	aat Asn	ctg Leu 270	gga Gly	gta Val	att Ile	816
ggc Gly	tat Tyr 275	gaa Glu	ccc Pro	aat Asn	aaa Lys	atg Met	acg Thr 280	agt Ser	gct Ala	gcg Ala	tat Tyr 285	gat Asp	tgg Trp	agg Arg	ctt Leu	864
gca Ala	tat Tyr 290	tta Leu	gat Asp	cta Leu	gaa Glu	aga Arg 295	cgc Arg	gat Asp	agg Arg	tac Tyr 300	ttt Phe	acg Thr	aag Lys	cta Leu	aag Lys	912
gaa Glu 305	caa Gln	atc Ile	gaa Glu	ctg Leu	ttt Phe 310	cat His	caa Gln	ttg Leu	agt Ser	ggg Gly 315	gaa Glu	aaa Lys	gtt Val	tgt Cys	tta Leu 320	960
att Ile	gga Gly	cat His	tct Ser	atg Met 325	ggg Gly	tct Ser	cag Gln	att Ile	atc Ile 330	ttt Phe	tac Tyr	ttt Phe	atg Met	aaa Lys 335	tgg Trp	1008
gtc Val	gag Glu	gct Ala	gaa Glu 340	ggc Gly	cct Pro	ctt Leu	tac Tyr	ggg Gly 345	aat Asn	ggg Gly	ggg Gly	cgt Arg	ggc Gly 350	tgg Trp	gtt Val	1056
aac Asn	gaa Glu	cac His 355	ata Ile	gat Asp	tca Ser	ttc Phe	att Ile 360	aat Asn	gca Ala	gca Ala	ggg Gly 365	acg Thr	ctt Leu	ctg Leu	ggc Gly	1104
gct Ala	cca Pro 370	aag Lys	gca Ala	gtt Val	cca Pro	gct Ala 375	cta Leu	att Ile	agt Ser	ggg Gly 380	gaa Glu	atg Met	aaa Lys	gat Asp	acc Thr	1152
att Ile 385	caa Gln	tta Leu	aat Asn	acg Thr	tta Leu 390	gcc Ala	atg Met	tat Tyr	ggg Gly 395	ttg Leu	gaa Glu	aag Lys	ttc Phe	ttc Phe	tca Ser 400	1200
aga Arg	att Ile	gag Glu	aga Arg	gta Val 405	aaa Lys	atg Met	tta Leu	caa Gln	acg Thr 410	tgg Trp	ggg Gly	ggg Gly	ata Ile	cca Pro	tca Ser 415	1248
atg Met	cta Leu	cca Pro 420	aag Lys	gga Gly	gaa Glu	gag Glu	gtc Val 425	att Ile	tgg Trp	ggg Gly	gat Asp	atg Met	aag Lys	tca Ser	tct Ser	1296

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tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att 1344
Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
      435                      440                      445

cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg 1392
Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
      450                      455                      460

aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa 1440
Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
      465                      470                      475                      480

aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa 1488
Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
      485                      490                      495

gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg 1536
Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
      500                      505                      510

gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac 1584
Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
      515                      520                      525

ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat 1632
Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
      530                      535                      540

gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct 1680
Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
      545                      550                      555                      560

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca 1728
Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
      565                      570                      575

atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776
Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
      580                      585                      590

att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824
Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
      595                      600                      605

ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
      610                      615                      620

gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
      625                      630                      635                      640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tcc cag 1968
Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
      645                      650                      655

atg ccc ttc cca atg taa 1986
Met Pro Phe Pro Met
      660

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<213> *Saccharomyces cerevisiae*

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Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly  
35 40 45  
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg  
50 55 60  
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu  
65 70 75 80  
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe  
85 90 95  
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe  
100 105 110  
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val  
115 120 125  
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn  
130 135 140  
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly  
145 150 155 160  
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val  
165 170 175  
Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile  
180 185 190  
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp  
195 200 205  
Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp  
210 215 220  
Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn  
225 230 235 240  
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile  
245 250 255  
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile  
260 265 270  
Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu  
275 280 285

Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys  
290 295 300

Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu  
305 310 315 320

Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp  
325 330 335

Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val  
340 345 350

Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly  
355 360 365

Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr  
370 375 380

Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser  
385 390 395 400

Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser  
405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser  
420 425 430

Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile  
435 440 445

Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met  
450 455 460

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln  
465 470 475 480

Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu  
485 490 495

Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met  
500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr  
515 520 525

Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp  
530 535 540

Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro  
545 550 555 560

Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser  
565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly  
580 585 590

Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp  
595 600 605

Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser  
610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp  
625 630 635 640

Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln  
645 650 655

Met Pro Phe Pro Met  
660

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<211> 2312  
<212> genomic DNA  
<213> Schizosaccharomyces pombe

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